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(without alignments)
19.309 Million cell updates/sec
                                                                                                               July 15, 2003, 12:51:16 ; Search time 10.6667 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   262574 seqs, 29422922 residues
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                         US-10-006-069A-55
35
1 DRSNLTR 7
                                                                                                                                                                                           Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                 Run on:
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1: /cgn2_6/ptodate/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/pcayBcytus_COMB.pep:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Issued_Patents_AA:*

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sednence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES	US-08-793-408-18	US-U9-139-762A-18 HS-09-187-789-43	US-09-139-600-38	-08	US-08-446-925-5	US-09-146-331-5	US-08-896-885-5	US-09-375-256-5	US-09-561-756-21	US-09-227-721-21	US-08-983-502-31	US-09-376-156-5	PCT-US96-10521-31	US-09-561-756-36	US-09-227-721-36	US-09-139-762A-72	US-09-139-762A-75	US-09-139-762A-93	US-08-842-306B-30	US-08-838-973B-30	US-08-771-212A-26	US-08-793-408-12	US-09-139-762A-12	US-08-188-277B-4	-429-964	US-09-357-251-35
DB	<u>.</u> د	۵ ۸	. 4	٣	-	7	~	4	4	4	4	4	Ŋ	4	4	m	m	ო	4	4	4	٣	m	7	7	4
Length		8 4	47	278	293	293	293	293	293	293	293	293	293	300	300	10	10	10	13	13	13	33	33	377	377	451
% Query Match	100.0	100.0	88.6	88.6	88.6		88.6	98.6	88.6	œ	88.6	88.6	9.88	88.6	88.6	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7
Score	35	3.13	31	31	31	31	31	31	31	31	31	31	31	31	31	30	30	30	30	30	30	30	30	30	30	30
Result No.	+ + (7 (4	2	9	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

100.0%; Score 35; DB 3; Length 89; 100.0%; Pred. No. 0.77;

Query.Match Best Local Similarity

Sequence 2, Appli Sequence 30, Appl Sequence 70, Appl Sequence 29, Appl Sequence 25, Appl Sequence 11, Appl Sequence 11, Appl Sequence 2, Appl		of DNA	
85.7 1523 4 US-09-182-024A-2 82.9 10 3 US-09-139-762A-30 82.9 10 3 US-09-139-762A-62 82.9 10 3 US-09-139-762A-70 82.9 13 4 US-08-818-973B-29 82.9 13 4 US-08-818-973B-29 82.9 276 4 US-08-195-11 82.9 377 1 US-08-195-12 82.9 377 2 US-08-195-23 82.9 377 2 US-08-125-11 82.9 377 2 US-08-125-11 82.9 377 2 US-08-125-11 82.9 377 1 US-08-139-14-80 82.9 377 2 US-08-22-617A-12 80.0 3666 2 US-08-22-617A-2 77.1 375 1 US-08-333-238-2	ALIGNMENTS	pplication US/08793408 7988 7988 Choo, Yen Riug, Aaron Sanchez Garcia, Isidro VENTION: Improvements in or Relating to VENTION: Binding Proteins for Recognition Sanchez Garcia Sidro Substance	
228 330 331 332 332 333 334 335 336 336 336 336 444 452 453 453 454 453 454 453 454 453 454 454		1 10.793.408 ence 18 ence 18 PPLICAN PAPLIC FILING P	
		RESULT C C C C C C C C C C C C C C C C C C C	

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TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING TITLE OF INVENTION: AND METHODS OF USE FILE REPERENCE: 480140.434c.
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43
LENGTH: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alnemri, Emad S.
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: AND METHOD OF USE
TITLE OF INVENTION: AND METHOD OF USE
FILE REFERENCE: 480140, 434
CURRENT APPLICATION NUMBER: US/09/139,600
CURRENT FILING DATE: 1998-08-25
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Pred. No. 2.9;
0; Mismatches 1; Indels
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Pred. No. 2.9;
0; Mismatches
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APPLICANT: Braxton, Scott M
APPLICANT: Diep, Dinh
TITLE OF INVENTION: HUMAN ICE HOMOLOG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3330 Hillview Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38, Application US/09139600 Patent No. 6432628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08522813 Patent No. 6033848
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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85.7%;
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SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                      ; ORGANISM: Mus musculus US-09-187-789-43
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12 DRDNLTR 18
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12 DRDNLTR 18
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Best Local Similarity
Matches 6; Conserv
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US-08-522-813-4.
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STATE:
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LENGTH: 47
                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Klug, Aaron
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
WUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pilisbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 89;
         0; Indels
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Pred. No. 0.77;
      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER:
BRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
BRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
BRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
BRIOR APPLICATION NUMBER:
APPLICATI
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
                                                                                                                                                                                                                                                                  Sequence 18, Application US/09139762A Patent No. 6013453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Application US/09187789; Patent No. 6340740; GENERAL INFORMATION: APPLICANT: Alnemri, Emad S.; APPLICANT: Fernandez-Alnemri, Teresa
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amino acid
   7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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ZIP: 20005-3918
COMPUTER READABLE FORM:
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74 DRSNLTR 80
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                                                            1 DRSNLTR 7
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US-09-187-789-43
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   Matches
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                                                                                                                                                                                                                                                                                                                            MCh2, AN APOPTOTIC CYSTEINE
PROTEASE, AND COMPOSITIONS FOR MAKING AND
METHODS OF USING THE SAME
                Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 293;
                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & ADDRESSEE: No. 5958720ris
STREET: One Liberty Place, 46th floor
CITI: Philadelphia
                  Score 31; DB 1;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB 2;
Pred. No. 22;
                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Worlderfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY MATE
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,239
REFERENCE/DOCKET NUMBER: TJU-1508
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/895,885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08896885
Patent No. 5985640
GENERAL INFORMATION:
APPLICANT: Litrack, Gerald
APPLICANT: Alnemri, Emad S.
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Litwack, Gerald
APPLICANT: Allomeri, Emad S.
APPLICANT: Fernandez-Allomeri, Te
TITLE OF INVENTION: Mch2, AN APC
TITLE OF INVENTION: METHODS OF UNUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                  Sequence 5, Application US/09146331
Patent No. 5958720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEO ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.6%;
85.7%;
                88.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 293 amino acids
amino acid
                Query Match
Best Local Similarity 85.77
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                           11 1111
70 DRDNLTR 76
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Best Local Similarity
Matches 6; Conserv
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                                                                                        1 DRSNLTR 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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US-08-896-885-5
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                                                                                                                                                                                                                                                                                                                                           Score 31; DB 3; Length 278; Pred. No. 20; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock, Washburn, Kurtz, Macklewicz & ADDRESSEE: No. 5672500ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHORIT, Teresa
Mch2, AN APOPTOTIC CYSTEINE
PROTEASE,
AND COMPOSITIONS FOR MAKING AND
METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Debluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1508
TELECOMMUNICATION INFORMATION:
TELEPAX: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF-0045P
TELECOMMUNICATION INFORMATION:
TELEPRIONE: 415-855-0155
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF USING THE SAME
TRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/522,813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08446925
Patent No. 5672500
GENERAL INFORMATION:
APPLICANT: Litwack, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Litwack, Gerald
Alnemri, Emad S.
Fernandez-Alnemri,
                                                                                                                                                                                                                                                                                                                                             88.6%;
85.7%;
                                                                                                                                                                                                                                : 278 amino acids
amino acid
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PROTITIES OF INVENTION: PROTITIES OF INVENTION: AND TITLE OF INVENTION: METH TITLE OF INVENTION: OF UNUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           Query Match 88.6
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-522-813-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-446-925-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alnemri,
                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                       DRDNLTR 61
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APPLICANT:
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                                                                                                                                                                                                                                LENGTH:
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Pred. No. 22;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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APPLICANT: Alnemri, Emad S.

TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/561,756
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 09/227,721
PRIOR FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/09227721
Patent No. 6379950
GENERAL INFORMATION: Bmad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 4;
Pred. No. 22;
0; Mismatches
                                                                                APPLICATION NUMBER: US/09/375,256
FILING DATE: 16-Aug-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                           NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1508
                                                                                                                                                      APPLICATION NUMBER: 08/446,925
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 116
SOFWARRE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 293
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                   TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/09561756 Patent No. 6376226
                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.6%;
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Best Local Similarity 85.،
ادر و Similarity 85.،
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 480140.431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo saplen
US-09-561-756-21
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70 DRDNLTR 76
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ALTILE OF INVENTION: MCh2, AN APOPTOTIC CYSTEINE
TITLE OF INVENTION: PROTEASE, AND COMPOSITIONS FOR MAKING AND
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
ADDRESSEE: One Liberty Place, 46th floor
CITY: Philadelphia
STREET: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 2; Length 293;
Pred. No. 22;
0; Mismatches 1; Indels
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AND COMPOSITIONS FOR MAKING AND
METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 6359127ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fernandez-Alnemri, Teresa
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/896,885
FILING DATE: 18-JUL-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1508
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3139
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,925
FILING DATE: 18-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09375256 Patent No. 6359127 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Litwack, Gerald Alnemri, Emad S.
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-896-885-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: David WALLACH
APPLICANT: Mark P. BOLLIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: YOLY V. GOLYSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES:
ADDRESSED: Browdy and Nelmark
                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                     Score 31; DB 4; Length 293;
Pred. No. 22;
0; Mismatches 1; Indels
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CONDITER: USA

CONDITER: FILOPY disk
MEDIUM TYPE: FILOPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SUSTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-JAN 1998
FILING DATE: 14-JAN 1996
FILING DATE: 14-JUN 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: II 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: II 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION NUMBER: II 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION NUMBER: II 115,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION NUMBER: II 115,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION NUMBER: II 117,932
FILING DATE: 17-DEC-1995
PRIOR APPLICATION NUMBER: II 117,932
FILING DATE: 17-DEC-1996
ATTONINEY/AGENT INFORMATION:
NAME: NAME: US-ARM-1996
ATTONINEY/AGENT INFORMATION:
NAME: NAME: 10-CALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Browdy and Neimark
419 Seventh Street N.W., Ste. 300
CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: EastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/08983502 Patent No. 6399327
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REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       88.6%;
85.7%;
                                                                                                                                                                                                                     Query Match 88.6
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                    1 DRSNLTR 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                      Score 31; DB 4; Length 293;
Pred. No. 22;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & ADDRESSEE: No. 6407215ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND COMPOSITIONS FOR MAKING AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MCh2, AN APOPTOTIC CYSTEINE TITLE OF INVENTION: PROTEASE, TITLE OF INVENTION: METHODS TITLE OF INVENTION: METHODS TITLE OF INVENTION: OF USING THE SAME NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/376,156
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Litwack, Gerald
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/446,925
                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09376156 Patent No. 6407215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Debuca: Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                          88.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (215) 568 3439
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 293 amino acids TYPE: amino acid
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                                                                                                                                      Query Match 88.6
Best Local Similarity 85.7
Matches 6; Conservative
                                                            ; TOPOLOGY: linear; KOLECULE TYPE: protein US-08-983-502-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
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70 DRDNLTR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 DRDNLTR 76
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                        1 DRSNLTR 7
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-376-156-5
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us-10-006-069a-55.rai

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MODULATORS OF THE FUNCTION OF FAS RECEPTORS AND OTHER PROTEINS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
; OTHER INFORMATION: Rev-Caspase-6 constructed from human caspase-6
US-09-561-756-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-561756-36

Sequence 36. Application US/09561756

Fatent No. 6376226

GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBIRANT, ACTIVE CASPASES AND USES:
TITLE REFERENCE: 480140.431

CURRENT APPLICATION NUMBER: US/09/561,756

PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 116

SOFTWARE: FESTERED for Windows Version 3.0

SEQ ID NO 36

LENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 293;
                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURREN APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DE
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-ARR-1996
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                  Sequence 31, Application PC/TUS9610521 GENERAL INFORMATION:
                                                       APPLICANT:
TITLE OF INVENTION: MODULATOR
TITLE OF INVENTION: AND OTHER
NUMBER OF SEQUENCES: 34
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPH disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
PCT-US96-10521-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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70 DRDNLTR 76
                                                                                                                                                                                                                                                                                                             FILING DATE:
PCT-US96-10521-31
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Ouery Match 88.6%; Score 31; DB 4; Length 300;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DRSNLTR 7
| | | | | | |
Db 191 DRDNLTR 197

Search completed: July 15, 2003, 12:56:08
Job time: 11.6667 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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· protein search, using sw model OM protein July 15, 2003, 12:48:06; Search time 33.3333 Seconds Run on:

(without alignments) 27.983 Million cell updates/sec

US-10-006-069A-68 36 1 RSDHLSR 7

Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 seqs, 133250620 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

/SIDS2/gggdata/geneseg/genesegp.embl/AA1989.DAT:*/SIDS2/gcgdata/geneseg/genesegp.embl/AA1990.DAT:*/SIDS2/gcgdata/geneseg/genesegp.embl/AA1991.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseqygeneseqp-embl/AA1981.DAT:*/SIDS2/gcgdata/geneseqygeneseqp-embl/AA1984.DAT:*/SIDS2/gcgdata/geneseqygeneseqp-embl/AA1985.DAT:*/SIDS2/gcgdata/geneseqygeneseqp-embl/AA1986.DAT:*/SIDS2/gcgdata/geneseqygeneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseqygeneseqp-embl/AA1987.DAT:*/SIDS2/gcgdata/geneseqp-embl/AA1988.DAT:*/SIDS2/gcgdata/geneseqygeneseqp-embl/AA1988.DAT:*/SIDS2/gcgdata/geneseqygeneseqp-embl/AA1988.DAT:*/SIDS2/gcgdata/geneseqp /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000 DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001 DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002 DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1992. /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1993. /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1994. /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1995. /SIDS2/gcgdata/geneseq/genesegp-embl/AA1996 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997 /SIDS2/gcgdata/geneseq/genesegp A_Geneseq_101002:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human KCA4 protein	Zinc protein recog	Amino acid sequenc	F3 zinc finger for	Human VEGF-targete					
Q:	AAE08729	AAB84235	AAB84247	ABB83583	ABJ03821	ABJ03825	ABJ03848	ABJ03858	ABJ03859	0000000
DB	22	22	22	23	23	23	23	23	23	ć
% Query Match Length DB ID	7	7	7	7	7	7	7	7	7	•
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	000
Score	36	36	36	36	36	36	36	36	36	,
Result No.		7	٣	4	S	9	7	8	σ	•

Human VEGF-targete Tuman VEGF-targete Human VEGF-targete Tuman VEGF-ta	inc finger inc finger inc finger
7 23 ABJ03861 7 23 ABJ03863 7 23 ABJ03866 7 23 ABJ03866 7 23 ABJ03870 7 23 ABJ03871 7 23 ABJ03871 7 23 ABJ03871 7 23 ABJ03897 7 23 ABJ03915 7 23 ABJ03915 7 23 ABJ03915 7 23 ABJ03915 7 23 ABB08019 7 23 ABB08019 7 23 ABB98016 7 23 ABB98016	3333
	36 100.0 36 100.0 36 100.0
1111. 1121. 1122. 1223. 1223. 1233. 1244. 1244. 1254.	4 4 4 5 4 5

ALIGNMENTS

AAE08729 standard; peptide; 7 AA. AAE08729;

RESULT 1

15-NOV-2001 (first entry)

Human KCA4 protein F3 recognition helix.

Human, KCA4; EPO; molecular target; zinc finger protein; ZFP; cellular process; signal transduction; drug-screening.

Homo sapiens

WO200159450-A2

16-AUG-2001.

08-FEB-2001; 2001WO-US04301

08-FEB-2000; 2000US-0181117

(SANG-) SANGAMO BIOSCIENCES ENC.

Case C;

WPI; 2001-522491/57.

Screening compound for interaction with molecular target by contacting compound with cells, comprising exogenous zinc finger protein that modulates expression of target, and determining values of properties of cells

7 AA;

us-10-006-069a-68.rag

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for identifying a gene or genes associated with a selected phenotype such as the one related to cancer, nephritis, prostate hypertrophy, hematopoiesis; osteoporosis, obesity, cardiovascular disease or diabetes. The method is useful in academic laboratories, in the biotechnological industries, and in pharmaceutical, genomic, agricultural and chemical companies. AAB84233.44 represent recognition helices of zinc finger proteins, which recognise different DNA triplets.
gene of interest, in cells exhibiting the phenotype. The method is useful
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                                                                              The invention relates to a method of screening a compound for interaction with a molecular target. The method involves contacting first and second cells with the compound and determining the values of properties of the compound. The second-cell comprises an exogenous zinc finger protein (ZPP) that modulates the expression of the molecular target, or isolating membranes from cell comprising SPP. The methods allow for high throughput screening of candidate compound and reduces the incidence of false positives. The methods are useful for screening a compound for interaction with a molecular target or for screening a compound for its effect on a cellular process. The method is useful for testing a compound for its capacity to transduce a signal to the molecular target or its and for performing blochemical drug-screening assays. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes a method for identifying genes associated with a selected phenotype. The method involves providing a library of nucleotide sequences encoding partially randomized zinc finger proteins, transducing cells with expression vectors, each comprising a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying genes associated with selected phenotype for research purposes, involves culturing cells transduced with nucleic acid encoding zinc finger proteins and assaying cells exhibiting selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phenotype associated gene; zinc finger protein; cancer; nephritis; prostate hypertrophy; hematopoiesis; osteoporosis; obesity; cardiovascular disease; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zinc protein recognition helix SBS3 for target DNA triplet GGG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 36; DB 22;
100.0%; Pred. No. 7.8e+05;
Live 0; Mismatches 0;
                      Sxample 10; Page 73; 99pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB84235 standard; peptide; 7 AA.
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tes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a method for identifying genes associated
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     purposes, involves culturing cells transduced with nucleic acid encoding zinc finger proteins and assaying cells exhibiting selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          companies. The present sequence represents a finger of a zinc finger protein.
                                                                                                                                                                                                                                                                                                                                               Phenotype associated gene; zinc finger protein; cancer; nephritis; prostate hypertrophy; hematopolesis; osteoporosis; obesity; cardiovascular disease; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying genes associated with selected phenotype for research
                                                    ö
                                                                                                                                                                                                                                                                                                               Amino acid sequence of finger 3 of a zinc finger protein.
                                                    Indels
                100.0%; Score 36; DB 22;
100.0%; Pred. No. 7.8e+05;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 41; 58pp; English.
                                                                                                                                                                                                             AAB84247 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                  (first entry)
Query Match
Best Local Similarity luv...
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                                                                                       1 RSDHLSR 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200140798-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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7 AA;

Sequence

from the library, culturing the cells for expressing the zinc finger protein, assaying the cells for selected phenotype, and identifying the

64

Query Match

Best Local Matches

ò g ABB83583

RESULT

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The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VBGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atheroscierosis, ischiaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention.
                                                                                diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatheroscierotic; vasotropic; antiathritic; vulneran antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetic retinopathy; psoríasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnera; antiulcer; cytostatic; antionipsoriatic; antidiabetic; ophthalmological; osteopathic; antilinfertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of gene and for treating atherosclerosis, ischemia, arthritis, wound or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human VEGF-targeted zinc finger protein fragment SEQ ID NO: 68
                                                                        protein; angiogenesis; vasculogenesis; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc finger protein; angiogenesis; vasculogenesis; ischaemia;
                                Human VEGF-targeted zinc finger protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eisenberg
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                      (SANG-) SANGAMO BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                           07-DEC-2000; 2000US-0733604.
12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
                                                                                                                                                                                                                                                                                       06-DEC-2001; 2001WO-US46861.
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25-SEP-2002 (first entry)
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Best Local Similarity
Matches 7; Conserv
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                                                                      finger
                                                                                                                                                                                                                                                       13-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                       Rebar E,
Jarvis E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a modified plant zinc finger protein. This zinc finger protein is used to modulated gene expression in a plant cell. Nucleic acid encoding the zinc finger is expressed in plant cells to produce a plant with an altered phenotype relative to the wild-type plant. The altered phenotype is high in nutritional value, yield, stress tolerance, pathogen resistance, resistance to agrochemicals, production of pharmaceutical compounds or production of industrial chemicals. The present sequence is a zinc finger protein sequence that is attracted to a ZFP target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified plant zinc finger protein for modulating gene expression in plant cell comprises zinc fingers that bind to a target site -
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                                                   Gaps
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               Length 7;
                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                Zinc finger; stress tolerance; pathogen resistance;
             Score 36; DB 22; Pred. No. 7.8e+05; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 36; DB 23;
larity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                             F3 zinc finger for target sequence ZFP 7.
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                                                                                                                                                                                                                ABB83583 standard; peptide; 7 AA.
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                                                 ;
           Similarity 100.0%; 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JAN-2002; 2002WO-US01906
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11-MAY-2001; 2001US-290716P.
                                                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-566792/60.
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                                                                                                             RSDHLSR 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200257294-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                   agrochemical
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ABJ0382

Eisenberg SP;

Wolffe A,

Liu P,

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30-APR-2001; 2001US-0846033.
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  Liu
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                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                            diabetic retinopathy or
shown in the invention.
  Jamieson A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jamieson A,
                              WPI; 2002-527918/56.
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                                                                                                                                                                                                           7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-2002
  Rebar E,
Jarvis E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rebar E,
Jarvis E;
                                                                                                                                                                                                            Sequence
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                                                                                  ulcer
                                                                                                                                                                                                                                                                                                                       RESULT 8
ABJ03858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2inc finger protein; anglogenesis; vasculogenesis; ischaemla;
diabetic retinopathy; psorlasis; arthropathy; cancer; tumour growth;
gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary;
antiulcer; cytostatic; antipsorlatic; antidiabetic; ophthalmological;
osteopathic; antiinfertility;
                                                                                                                                                                         New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of the gene and for treating atherosclerosis, ischemia, arthritis, wound or
                                                                                                                                                                                                                                               The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention.
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                                                                                                                         Wolffe A, Eisenberg SP;
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                                                                                                                                                                                                                                                                                                                                                     Length 7;
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                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 36; DB 23;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
                                                                                                                         Liu P,
                                                                                                                                                                                                                            Claim 4; Page 102; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABJ03848 standard; Peptide; 7 AA.
                                                                                                    (SANG-) SANGAMO BIOSCIENCES INC
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                                                                                                                        Jamieson A, Liu Q,
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12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
                                                                     12-DEC-2000; 2000US-0736083.
                                       06-DEC-2001; 2001WO-US46861
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nes 7; Conser
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WO200246412-A2.
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                                                           07-DEC-2000;
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                   13-JUN-2002
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                                                                                                                       Rebar E,
Jarvis E;
                                                                                                                                                                                                                                                                                                                                Sequence
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diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary; antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological;
                                                                                                                                                                                                                                                                                                The present invention relates to a zinc finger protein that binds to a target site in one or more vasular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide
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New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of t gene and for treating atherosclerosis, ischemia, arthritis, wound or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; angiogenesis; vasculogenesis; ischaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 36; DB 23; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                    Claim 4; Page 102; 195pp; English.
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The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnera antiulcer; cytostatic; antiatissoriatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of tgene and for treating atherosclerosis, ischemia, arthritis, wound or
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Human VEGF-targeted zinc finger protein fragment SEQ ID NO: 102.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; angiogenesis; vasculogenesis; ischaemia;
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                                                                                                                                   100.0%; Score 36; DB 23; Length 7
100.0%; Pred. No. 7.8e+05; ....matches 0; Indels
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Pred. No. 7.8e+05;
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100.0%;
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2001US-0846033.
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jamieson A,
                                                                                                                                   Query Match
Best Local Similarity
7; Conserve
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30-APR-2001;
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Jarvis E;
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetic retinopathy, psoriasis, arthropathy; cancer, tumour growth, gene therapy, antiatherosclerotic, vasotropic, antiarthritic, vulnera) antiulcer; cytostatic, antipsoriatic, antidiabetic, ophthalmological,
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Gaps
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   Indels
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Pred. No. 7.8e+05;
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   Mismatches
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12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
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(SANG-) SANGAMO BIOSCIENCES INC.
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Jarvis E;
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Matches
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                                                    linc finger protein; angiogenesis; vasculogenesis; ischaemia; diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary; anticler; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antilnfertility.
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                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischaemia, arthritis, wounds, uicers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention.
                                                                                                                                                                                                                                                                                                                                 New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of the gene and for treating atherosclerosis, ischemia, arthritis, wound or ulcer
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                                Human VEGF-targeted zinc finger protein fragment SEQ ID NO: 104
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RSDHLSR 7
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Zinc finger protein; anglogenesis; vasculogenesis; ischaemia; diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiathritic; vulnerary; antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                  New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of t gene and for treating atherosclerosis, ischemia, arthritis, wound or
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                                                                                                                                                                                                                                                                 Liu 0,
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12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
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06-DEC-2001; 2001WO-US46861.
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The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used trreat atheroscierosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention.

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gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary;
antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological;
                                                                                                                                                                          The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating anglogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide
                                                                             New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of the gene and for treating atherosclerosis, ischemia, arthritis, wound or
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           Eisenberg SP;
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tive 0; Mismatches 0;
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           Liu
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           Jamieson A,
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7; Conserve
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Jarvis E;
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Jarvis E;
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                                                                                                                                           100.0%; Score 36; DB 23;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
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Jarvis E;
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Length 7;

23;

ВВ

100.0%; Score 36;

Query Match

Claim 4; Page 102; 195pp; English.

0; Gaps Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 7; Conservative 0; Mismatches 0; Indels

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1 RSDHLSR 7

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Search completed: July 15, 2003, 12:53:01 Job time: 34.6667 secs

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OM protein - protein search, using sw model

July 15, 2003, 12:49:31; Search time 6.66667 Seconds (without alignments) 43.550 Million cell updates/sec Run on:

US-10-006-069A-247 36 1 TSGHLSR 7

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•	Description	Sac	Q03125 saccharomyc	P78768 schizosacch	P42705 canis famil	P20501 vaccinia vi	P12926 vaccinia vi	O08537 mus musculu	rattı	Q9bxb4 homo sapien	homo	Q9hfr7 trichoderma	Q53158 rhodobacter	Q04832 leishmania		042395 gallus gall			Q9hgp5 schizosacch		P22464 drosophila	Q00055 saccharomyc	_		Q8yjj7 brucella me	Q9ybk6 aeropyrum p	P27214 bos taurus		P33477 oryctolagus	homo sap	. Q92125 xenopus lae		P45205 haemophilus	O15945 drosophila
SUMMARIES	QI	NRG2_YEAST	NRG1_YEAST	VTI1_SCHPO	TPO_CANFA	VI07_VACCC	VIO7_VACCV	ESR2_MOUSE	ESR2_RAT	ORPB_HUMAN	RIN1_HUMAN	RL36_TRIHM	HIS3_RHOSH	HEXP_LEIMA	CNBP_MOUSE	CNBP_CHICK	CNBP_HUMAN	GLO2_BUCAI	CAPB_SCHPO	ANX5_CHICK	ANX9_DROME	GPD1_YEAST	ANX7_MOUSE	ANX7_HUMAN	ARLY_BRUME	SYC_AERPE	ANXB_BOVIN	ANXB_MOUSE	ANXB_RABIT	ANXB_HUMAN	ANX7_XENLA	ANX6_BOVIN	DXS_HAEIN	ARNT_DROME
	DB	П	Н	Н	Н	Н	Н	Н	-	Н	٦	Н	Н	-	Н	7	-	Н	_	٦	7	Н	7	-	П	-	7					-	Α,	-
	Query Match Length	220	231	214	352	423	423	530	530	747	783	105	119	271	170	172	177	251	268	321	324	391	463	466	466	475	203	503	503	505	512	618	625	644
ð	Query Match	100.0	91.7	88.9	86.1	86.1	86.1	86.1	86.1	ė.		90.6	90.6	90.6	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8					•	77.8	77.8	77.8
	Score		33	32	31	31	31	31	31	31	30	59	59	53	. 82	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	58	28
	Result No.	7	7	m	4	ഗ	9		80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	ε ε

P48037 rattus norv	Q44737 borrelia bu	P97435 mus musculu	Q9z0ul mus musculu	P02243 tachypleus	Q56353 paracoccus	Q99qd5 staphylococ	P57576 buchnera ap	P36627 schizosacch	Q9kad3 bacillus ha	Q914p1 staphylococ	P76657 escherichia	
ANX6_RAT	CHEA_BORBU	ENTK_MOUSE	ZOZ_MOUSE	HCYA_TACTR	YNAC_PARPN	MSA1_STAAM	RL6_BUCAI	BYR3_SCHPO	LEXA_BACHD	LEXA_STAAU	YQIJ_ECOLI	
-	Н	Ч	Н	Н	Н	-	Н	Н	+4	-	-	
672	864	1069	1167	87	97	169	178	179	207	207	209	
77.8	77.8	77.8	77.8	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	
28	28	28	28	27	27	27	27	27	27	27	27	
34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

ALIGNMENTS NDARD; PRT; 220 AA. 30, Created) 30, Last sequence update) 40, Last annotation update) 40, Last annotation update) 40, Last annotation update) 41, Lonal regulator NRG2. 42, Seder's yeast) 43, Eaker's yeast) 43, Eaker's yeast) 53, Saccharomycotina; Saccharomyces 53, Saccharomycetaceae; Saccharomyces 53, Saccharomycetaceae; Saccharomyces 64, Schwarzlose C., Vetter I.; 74) to the EMBL/GenBank/DDBJ databases. 75, STRPTIONAL REPRESSOR (BY SIMILARITY) 70, SATIONAL REPRESSOR (BY SIMILARITY) 71, SATIONAL REPRESSOR (BY SIMILARITY) 72, STRIPTIONAL REPRESSOR (BY SIMILARITY) 73, SATIONAL REPRESSOR (BY SIMILARITY) 74, SATIONAL REPRESSOR (BY SIMILARITY) 75, SATIONAL REPRESSOR (BY SIMILARITY) 76, SATIONAL REPRESSOR (BY SIMILARITY) 77, SATIONAL REPRESSOR (BY SIMILARITY) 78, SATIONAL REPRESSOR (BY SIMILARITY) 79, SATIONAL REPRESSOR (BY SIMILARITY) 70, SATIONAL SA LONG S	les 7; Conservative 0; Mismatch
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNAS
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMED outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                         Park S.H., Hwang H.J., Kang H.S.; "MSSI gene, encoding a zinc-finger motif, is involved in glucose repression and STA10 repression of glucoamylase gene in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                               Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR INVOLVED IN REGULATION OF GLUCOSE REPRESSION. BINDS TO UAS-1 IN THE STAI PROMOTER.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                        16-02T-2001 (Rel. 40, Created)
16-02T-2001 (Rel. 40, Last sequence update)
16-02T-2001 (Rel. 40, Last sequence update)
16-02T-2001 (Rel. 40, Last annotation update)
17 transcriptional regulator NRG1 (Zinc finger protein MSS1).
NRG1 OR MSS1 OR YDR043C OR YD5112.01C.
Saccharomyces cerevisiae (Baker's great).
Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetaes; Saccharomycetales;
                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
Oliver K., Harris D., Barrell B., Rajandream M.A., Walsh S.V.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.7%; Score 33; DB 1; Length 231; 85.7%; Pred. No. 4.5;
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                                                        231 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: STRONG, TO NRG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIII_SCHPO
ID VTII_SCHPO STANDARD;
AC P78768; 043039;
DT 15-JU1-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 85.7
les 6; Conservative
                                                        STANDARD;
164 TSGHLSR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 TSGHLAR 191
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TSGHLSR 7
                                                                                                                                                       NCBI_TaxID-4932;
                                                                                                                                                                                                                                    STRAIN-AN20-5B;
                                                       NRG1_YEAST
Q03125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                               NRG1_YEAST
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RAM WOOD V. GWilliam R., Radaltabysov,
RAM Wood V., GWilliam R., Radaddram M.A., Lyne M., Lyne R., Stewart A.,
RA Sqouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chilingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Rad Collins M., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Goliver K., O'Neil S., Pearson D., Quali M.A., Rabbinowitsch E.,
RA Skelton J., Simmonds M., Squares R., Squares S.,
Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Skelton J., Volnstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Radibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
A Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gelzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Galzon A., Thode G.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
R. The genome sequence of Schizosaccharomyces pombe.";
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-!- FUNCTION: V-SNARE THAT MEDIATES VESICLE TRANSPORT PATHWAYS THROUGH
-!- FUNCTIONS WITH T-SNARES ON THE TARGET MEMBRANE. THESE
INTERACTIONS ARE PROPOSED TO MEDIATE ASPECTS OF THE SPECIFICITY OF
VESICLE TRAFFICKING AND TO PROMOTE FUSION OF THE LIPID BILAYERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98162722; PubMed-9501991;
Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
"Identification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
Q -> H (IN REF. 2).
; 641A57E4D7E52A6F CRC64;
                                                                                                                                                                                                            Eukaryota; Fungī; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                     Vesicle transport v-SNARE protein VIII homolog
SPBC3B9.10.
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00397; t_SNARE; 1.
Transmembrane; Transport; Protein transport.
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                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21848401; PubMed-11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL022070; CAA17790.1; -. EMBL; D89116; BAA13778.1; -. InterPro; IPR000727; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24743 MW;
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                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896;
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Late protein
                                                                                                                                           01-FEB-1991
16-OCT-2001
                                                                        v107_VACCC
P20501:
                                                                                                                          01-FEB-1991
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6
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P12926;
                                                                                                                                                                                       Protein 17
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                                                               VIO7_VACCC
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                                           RESULT 5
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AND MATURATION OF MEGAKARYOCYTES FROM THEIR COMMITTED PROGENITOR
CELLS. IT ACTS AT A LATE STAGE OF MEGAKARYOCYTE DEVELOPMENT. IT
MAY BE THE MAJOR PHYSIOLOGICAL REGULATOR OF CIRCULATING PLATELETS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: TWO-DOMAIN STRUCTURE WITH AN ERYTHROPOIETIN-LIKE N-
TERMINAL AND A SERF PRO/THR-RICH C-TERMINAL.
-!- SIMILIARITY: BELONGS TO THE EPO / TPO FAMILY.
InterPro; IPR001323; EPO_TPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification and cloning of a megakaryocyte growth and development factor that is a ligand for the cytokine receptor Mpl."; cell 77:1117-1117(1994).
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bartley T.D., Bogenberger J., Hunt P., Li Y.-S., Lu H.S., Martin F., Chang M.-S., Samal B.B., Nichol J.L., Swift S., Johnson M.J., Hsu R.-Y., Parker V.P., Suggs S., Skrine J.D., Merewether L.A., Clogson C., Hsu E., Hokom M.M., Hornkohl A., Choi E., Pangelinan M., Sun Y., Mar V., McNich J., Simonet L., Jacobsen F., Xie C., Shutter J., Chute H., Basu R., Selander L., Trollinger D., Sieu L., Padilla D., Trail G., Elliott G., Izuni R., Covey T., Crouse J., Padilla A., Xu W., del Castillo J., Biron J., Cole S., Hu M.C.-T., Pacifici R., Ponting I., Saris C., Wen D., Yung Y.P., Lin H.,
                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Thrombopoletin precursor (Megakaryocyte colony stimulating factor)
(C-NEL ligand) (ML) (Megakaryocyte growth and development factor)
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
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(POTENTIAL).
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19;
Indels
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                                                                                                                                                                                     352 AA.
  Mismatches
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PROSITE; PS00817; EPO_TPO; 1.
Cytokine; Glycoprotein; Hormone; Signal.
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Pred. No.
                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.1%;
Similarity 85.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00758; EPO_TPO; 1
6; Conservative
                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23
352
1172
1172
1195
206
234
255
332
                                                                 169 TSGHLDR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347
352 AA;
                                     1 TSGHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                      THPO OR TPO.
                                                                                                                                                                                     TPO_CANFA
P42705;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                       MGDF)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDIAGE-2835495; MEDIAGE-1815015; Pubwed-2835495; Schmitt J.F.C., Stunnenberg H.G.; "Sequence and transcriptional analysis of the vaccinia virus HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccinia virus (strain WR).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                    Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                             MEDINE=91021027; PubMed=2219722;
Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paolettí E.;
                                                                                                                                                                                                                                                                                                                                                                                                                            Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P., Paoletti E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Appendix to 'The complete DNA sequence of vaccinia virus'."; Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 AA; 49039 NW; 633F501637FD80D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE POXVIRUSES I7 FAMILY
                                                                                                                                                                                                                                                                                                                                          "The complete DNA sequence of vaccinia virus."; virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 1;
Pred. No. 23;
); Mismatches 0
                                      (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004970; Peptidase_C57.
Pfam; PF03290; Peptidase_C57; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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100.0%; Pr∈
0; 7
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(Rel. 12, Last sequ
(Rel. 40, Last anno
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PIR; C42511; C42511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 SGHLSR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SGHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10254;
                                                                                                                                                                                                                 NCBI_TaxID=10249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; C57.001;
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLETE GENOME
                                                                                                                                                                                               Orthopoxvirus
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01-OCT-1989 (
15-OCT-2001 (
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SEQUENCE OF 1-60 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          ALPHA.
                                                                                                                                                                                                                                                                                      mice."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-129/Sv; TISSUE-Ovary;
MEDLINE-97211383; PubMed-9058381;
Tremblay G.B., Tremblay A., Copeland N.G., Gilbert D.J., Jenkins N.A., Labrie F., Giquere V.;
"Cloning, chromosomal localization, and functional analysis of the murine estrogen receptor beta.";
Mol. Endocrinol. 11:353-365(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pettersson K., Grandien K., Kuiper G.G.J.M., Gustafsson J.-A.; "Mouse estrogen receptor beta forms estrogen response element-binding heterodimers with estrogen receptor alpha."; Mol. Endocrinol. 11:1486-1496(1997).
                                                      Fathi Z., Condit R.C.; "Genetic and molecular biological characterization of a vaccinia virus temperature-sensitive complementation group affecting a virion
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Ovary;
Leygue E., Lu B., Dotzlaw H., Glor C., Watson P.H., Murphy L.C.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
[4]
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                                                                                                                                                                                                                                                                                                                 86.1%; Score 31; DB 1; Length 423; 100.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                6EB5BF25D7FD9FEE CRC64;
                                                                                                   Virology 181:258-272(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 46-530 FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           ESR2_MOUSE STANDARD; PRT; 530 AA. 008537; 035635; 070519; 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 34, Last sequence update) 15-JUL-2002 (Rel. 41, Last annotation update) ESR1096n receptor beta (ER-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 46-530 FROM N.A., AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 23; ive 0; Mismatches
                                                                                                                                                                                                                                                          InterPro; IPR004970; Peptidase_C57.
Pfam; PF03290; Peptidase_C57; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97424142; PubMed-9280064;
                                             MEDLINE-91134989; PubMed-1994576;
                                                                                                                                                                                                                                                                                             423 AA; 49010 MW;
 I fragment.";
J. Virol. 62:1889-1897(1988).
                                                                                                                                                                                                                            EMBL; J03399; AAB59809.1; -
                                 SEQUENCE OF 1-215 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-60 FROM N.A.
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                       PIR; G29889; WZVZI7.
PIR; A38497; A38497
                                                                                                                                                                                                                                                                                                                              Similarity
6; Conserva
                                                                                                                                                                                                                                                                                                                                                                              SGHLSR 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Ovary;
                                                                                                                                                                                                                                                                                     Late protein
                                                                                           component.
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                    ESR2_MOUSE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLICING.
-1- TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, OVARY, LEYDIG CELLS AND IN EPITHELIUM OF THE EFFERENT DUCTULES AND OF THE INITIAL SEGMENT OF THE EPIDIDYMIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
NR3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endocrinology 139:2982-2987(1998).
-I- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
-I- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
                                                                                                                                                                                                      MEDLINE-20450734; PubMed-10995228; Cheng X., Cole R.N., Zaia J., Hart G.W.; "Alternative O-glycosylation/O-phosphorylation of the murine estrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Transcription and translation of estrogen receptor-beta in the male reproductive tract of estrogen receptor-alpha knock-out and wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lu B., Leygue E., Dotzlaw H., Murphy L.J., Murphy L.C., Watson P.H.; "Estrogen receptor-beta mRNA variants in human and murine tissues."; Mol. Cell. Endocrinol. 138:199-203(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS; BETA-1 (SHOWN HERE),
BETA-2, BETA-5, BETA-5A AND BETA-6; ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                        CARBOHYDRATE-LINKAGE SITE SER-61, AND PHOSPHORYLATION SITE SER-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00399; ZNF_C4; 1.
PROSITE; PS00031, NUCLEAR_ERCEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
Zinc-finger; Steroid-binding; Alternative splicing; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98268825; PubMed-9607809;
Rosenfeld C.S., Ganjam V.K., Taylor J.A., Yuan X., Stiehr J.R.,
Hardy M.P., Lubahn D.B.;
STRAIN-C57BL/6J x 129; TISSUE-Ovary;
Rosenfeld C.S., Lubahn D.B.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tather Pro: IPR000536; Hormone_rec_11g.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
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EMBL; AF067422; AAC17919.1; ALT_INIT.
EMBL; AF063853; AAC16656.1; -.
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PRINTS; PR00047; STROIDFINGER.
PRODOM; PD000035; Znf_G4steroid; 1.
                                                                                                                                                                                                                                                                                                                                                                      Biochemistry 39:11609-11620(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Ovary;
MEDLINE=98348389; PubMed=9685228;
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Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U81451; AAB51132.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00430; HOLI;
SMART; SM00399; ZNF_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P03372; 1HCQ.
                                                                                                                                                                                                                                                                                                                                            receptor beta.
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us-10-006-069a-247.rsp

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                            S->A: NO LOSS OF THE STIMULATORY EFFECT OF RAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 46-530 FROM N.A. (ISOFORM BETA-1).
STRAIN-Sprague-Dawley; TISSUE-Prostate;
MEDLINE-96534066; PubMed-8650195;
Kujber G.G.J.M., Enmark E., Pelto-Huikko M., Nilsson S.,
Gustafsson J.-A.;
"Cloning of a novel receptor expressed in rat prostate and ovary.";
Proc. Natl. Acad. Sci. U.S.A. 93:5925-5930(1996).
                                                                                                                                                     MISSING (IN ISOFORM BETA-5).
MISSING (IN ISOFORM BETA-6).
MISSING (IN ISOFORM BETA-5A).
S-A: ABOLISHES STIMULATORY EFFECT OF
                                                                         PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY MAPK) (PROBABLE).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A novel isoform of rat estrogen receptor beta with 18 amino acid insertion in the ligand binding domain as a putative dominant negative regular of estrogen action."; Biochem. Blophys. Res. Commun. 246:142-147(1998).
                                                                                                                                 --> RSSEDPHWHVAQTKSAVPR (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Wistar; TISSUE=Ovary;
MEDLINE=98262932; PubMed=9600083;
Maruyama K., Endoh H., Sasaki-Iwaoka H., Kanou H., Shimaya E.,
Hashimoto S., Kato S., Kawashima H.;
                                                                                                                                                                                                                                                                                                                                  DB 1; Length 530; 30;
                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              G6286; O70195; O35785; O55015; O55016; O35784; Q9R185; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update) Estrogen receptor beta (ER-beta).
                                                                                                                                                                                                                                                                                      -> R (IN REF. 2).
-> G (IN REF. 2).
90E73A161550ABE4 CRC64;
                    NUCLEAR RECEPTOR-TYPE. C4-TYPE.
                                                                                                           (GLCNAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 46-530 FROM N.A. (ISOFORM BETA-2).
                                                    STEROID-BINDING PHOSPHORYLATION
                                                                                                                       /FTId-CAR_000201
                                                                                                                                                                                                                                  (IN REF.
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                   Score 31;
Pred. No.
                                                                                                             O-LINKED
                                                                                                                                                                                                                                 ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM BETA-2).
STRAIN=Wistar; TISSUE-Prostate;
                                                                                                                                                                                                                                                                                                                          86.1%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                             59012 MW;
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   norvegicus (Rat)
                                                                                                                                                                 604
                                                                                                                                                                                                                                           142
200
378
412
445
511
          148
214
214
169
209
530
61
87
105
488
                                                                                                                                364
                                                                                                                                                                                                                                                                                      445
511
530 AA;
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           |||||||
82 TSGHLS 87
                                                                                                                                                                                                                                                                                                                                                                             1 TSGHLS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10116;
                                                                                                                                                     319
365
319
105
                                                                61
87
105
488
61
Phosphorylation
                                                                                                                                364
                   DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                           CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                  VARSPLIC
                                                   DOMAIN
MOD_RES
MOD_RES
MOD_RES
                                                                                                          CARBOHYD
                                                                                                                                VARSPLIC
                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                 CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBCELLULAR LOCATION: Nuclear.
-:- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS; BETA-1 (SHOWN HERE),
BETA-1/DELTA-3, BETA-1/DELTA-4, BETA-2 AND BETA-2/DELTA-3; ARE
PRODUCED BY ALTERNATIVE SPLICING.
-:- TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, OVARY, LUNG, LIVER,
KIDNEY, FAT, BONE, BRAIN, UTERUS AND TESTIS.
-:- DOMAIN: COMPOSED OF THREE DOMAINS: A MODILATING N-TERMINAL DOMAIN,
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-:- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
NR3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                    brain.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!-FÜNCTION: BINDS ESTRGEENS WITH AN AFFINITY SIMILAR TO THAT OF ER-
-!-FÜNCTION: BINDS ESTRGESSION OF REPORTER GENES CONTAINING
ESTRGEEN RESPONSE ELEKENTS (ERE) IN AN ESTRGEN-DEPENDENT MANNER.
ISOFORMS BETA-1/DELTA-3 AND BETA-2/DELTA-3 ARE UNABLE TO BIND DNA
AND ACTIVARE TRANSCRIPTION DUE TO THE TRUNCATION OF THE DNA
BINDING DOMAIN. ISOFORM BETA-2 SHOWS LOSS OF LIGAND BINDING
AFFINITY AND SUPPRESSES ER-ALPHA AND ER-BETA-1 MEDIATED
TRANSCRIPTIONAL ACTIVATION AND MAY ACT AS A DOMINANT NEGATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGULATOR OF ESTROGEN ACTION.
SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
ALPHA. CAN ALSO FORM HETERODIMERS BETWEEN ISOFORMS BETA-1 AND
               "Tissue specific responses to estrogen: an explanation based on differential activation of multiple estrogen receptors with different estrogen response elements."; submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                             Brown T.A.; "Identification of estrogen receptor beta2, a functional variant of estrogen receptor beta expressed in normal rat tissues."; Endocrinology 139:1082-1092(1998).
                                                                                                                        SEQUENCE OF 46-530 FROM N.A. (ISOFORMS BETA-1; BETA-2; DELTA-3)
                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1/DELTA-4).
STRAIN-Spraque-Dawley; TISSUE-Brain;
Price R., Handa R.J.
"A novel splice variant of estrogen receptor beta found in rat
                                                                                                                                                                                         Petersen D.N., Tkalcevic G.T., Koza-Taylor P.H., Turi T.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR00035; Hormone_rec_11g.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pf00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0047; STROIDFINGER.
PRODOM; PRO00035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                               STRAIN-Sprague-Dawley;
MEDLINE-98151005; PubMed-9492041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00398; STRDHORMONER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U57439; AAC52602.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF042058; AAB97424.1;
EMBL; AF042059; AAB97425.1;
EMBL; AF042060; AAB97426.1;
EMBL; AF042061; AAB97427.1;
EMBL; AF161187; AAD47637.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P03372; 1HCQ
Aldridge T.C.;
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InterPro; IPR001849; PH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Oxysterol binding protein-related protein 11 (OSBP-related protein 11)
                                                                                                                                                                                                                                                                                                                    Gaps
otion regulation; DNA-binding; Nuclear protein; id-binding; Alternative splicing; Phosphorylation.
                                                                                                PHOSPHORYLATION (BY SIMILARITY).
PHOSPHOKYLATION (BY SIMILARITY).
MISSING (IN ISOPORM BETA-1/DELTA-3 AND
ISOPORM BETA-2/DELTA-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21601154; Pubmed-11735225; Madorski C.J., Morotata E., Li A., Lee R., Rodriguez I.R.; Radorski C.J. Li A., Lee R., Redriguez I.R.; A family of 12 human genes containing oxysterol-binding domains."; Genomics 78:185-196(2001).
                                                                                                                                                       MISSING (IN ISOFORM BETA-1/DELTA-4).

R -> RSSEDPHWHYA, MRSAAPR (IN ISOFORM BETA-2, AND ISOFORM BETA-2/DELTA-3).

L -> Q (IN REF. 3 AND 4).

P -> A (IN REF. 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21376257; PubMed-11483621;
Lehtco M., Laitinen S., Chinetti G., Johansson M., Ehnholm C., Staels B., Ikonen E., Olkkonen V.M.;
"The OSBP-related protein family in humans.";
J. Lipid Res. 42:1203-1213(2001).
-1- TISSUE SPECIFICITY: Widely expressed.
-1- SIMILARITY: BELONGS TO THE OSBP FAMILY.
                                                                                                                                                                                                                              S -> P (IN REF. 3; CAA05631).
S -> P (IN REF. 3; CAA05631).
36F269D9FD773DA9 CRC64;
                                                                                                                                                                                                                                                                                        Score 31; DB 1; Length 530;
                                                                                                                                                                                                                                                                                                                    0; Indels
                                           NUCLEAR RECEPTOR-TYPE
                                                                      C4-TYPE.
STEROID-BINDING
                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 30; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:16397; OSBPL11.
MIM; 606739; -.
InterPro; IPR000648; Oxysterol_BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF392454; AAL40667.1; -. EMBL; AF346292; AAK31141.1; -.
                                                                                                                                                                                                                                                           59152 MW;
                                                                                                                                                                                                                                                                                        86.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSBPL11 OR ORP11 OR OSBP12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:16397; OSBPL11
                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
  Receptor; Transcription
                                                                                                                                                       318
364
                                                                                                                                                                                                 72
150
165
505
530 AA;
                 Zinc-finger; Steroi
                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              TSGHLS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             1 TSGHLS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                           149
149
185
215
87
488
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORPB_HUMAN
                                         DNA_BIND
ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                               MOD_RES
MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                         VARSPLIC
                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
ORPB_HUMAN
                                                                                                                                                                                                                                                                                                                 Matches
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REDINE-97289700; PUBMEd-9144171;

MEDLINE-97289700; PUBMEd-9144171;

MILLE O., Colicelli J.;

MILLE O., Colicelli J.;

MILLE O., Colicelli J.;

Protein binding and signaling properties of RINI suggest a unique effector function...;

Protein binding and signaling properties of RINI suggest a unique effector function...;

Protein binding and signaling properties of RINI suggest a unique effector function...;

Protein Mai INTERERE WITH RAS FUNCTION INTERACTS DIRECTLY

WITH RAS AND COMPETES WITH RAPI IN YEAST. FUNCTIONS AS AN EFFECTOR OR REGULATOR OF RAS. MAY ALSO INTERACT WITH 14-3-3 PROTEINS AND PROTEINS CONTAINING SH3 DOMAINS.

-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; RINI (SHOWN HERE) AND RINI-

DELTA; ARE PRODUCTS: 2 ISOFORMS; RINI (SHOWN HERE) AND RINI-

TIEVELS IN BRAIN, PLACEMAN AND PANCEMAS.

-I TISSUES SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED WITH HIGH LEVELS IN BRAIN, PROBABLY PHOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFFECTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIN1-DELTA SHOWS REDUCED ABILITY TO BIND TO RAS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression of three mammalian cDNAs that interfere with RAS function
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colicelli J., Nicolette C., Birchmeler C., Rodgers L., Riggs M.,
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A human protein selected for interference with Ras function interacts directly with Ras and competes with Rafl."; Mol. Cell. Biol. 15:1318-1323(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     013671; Q00427; O15010;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNY-2002 (Rel. 41, Last annotation update)
Ras interaction/interference protein 1 (Ras inhibitor JC99).
                                                                                                                                                                                                                                                                                                       Length 747;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Han L., Colicelli J.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                        B443D3BDE8AE5FB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in Saccharomyces cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 88:2913-2917(1991).
                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                   86.1%; Score 31; DB : 100.0%; Pred. No. 43; tive 0; Mismatches
Pfam; PF00169; PH; 1.
Pfam; PF01237; Oxysterol_BP; 1.
SMART; SM00233; PH; 1.
PROSTIE; PS01013; OSDP; FALSE_NEG.
PROSTIE; PS0003; PH_DOMAIN; 1.
Lipid transport; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRÉLIMINARY SEQUENCE FROM N.A.
MEDLINE-95166216; Pubmed-7862125;
Han L., Colicelli J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Glial cell;
MEDLINE-91187901; PubMed-1849280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND REVISIONS
                                                                                                                                                                                                                                     SEQUENCE 747 AA; 83643 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Glioblastoma;
Han L., Colicelli J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo saptens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 TSGHLS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- MISCELLANEOUS: 14-3-3 PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TSGHLS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIN1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wigler M.;
                                                                                                                                                                                                                                                                                                       Query Match
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RIN1_HUMAN
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HEXP_LEIMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
SIMILARITY: TO OTHER MAMMALIAN RAS INHIBITORS AND TO YEAST VPS9. SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAS AND 14-3-3 PROTEIN BINDING REGION. MISSING (IN ISOFORM RIN1-DELTA). DIFC1392295127A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fekete C., Posta K., Hornok L.; Isolation and characterization of a Trichoderma hamatum ribosomal protein gene, TRP36."; Districted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE L36E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fung1; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Trichoderma.
NCBI_TaxID=49224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.3%; Score 30; DB 1; Length 783; 71.4%; Pred. No. 75; 1.4%; Pred. 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
60S ribosomal protein L36 (TRP36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF308443; AAG28787.1; -.
InterPro; IPR00509; Ribosomal_Li36e.
Pfam, PF01158; Ribosomal_Li36e; 1.
ProDom; PD009192; Ribosomal_Li36e; 1.
PROSITE; PS01190; RIBOSOMAL_Li36E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                            InterPro; IPR000159; RA_domain.
InterPro; IPR000980; SH2.
                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00017; SH2; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF02204; VPS9; 1.
SWART; SW0014; RA; 1.
SWART; SW00167; VPS9; 1.
PROSITE; PS50001; SH2; 1.
SH2 domain; Phosphorylation; Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            783 AA; 84117 MW;
                                                                                                                                                                                                                                                 EMBL; L36463; AAB67270.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|||:|
21 TTGHLAR 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trichoderma hamatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
Les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TSGHLSR 7
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                                                                                                                                                                                                                                                                            MIM; 605965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RL36_TRIHM
Q9HFR7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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SO THE TENT OF THE PROPERTY OF
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                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                ö
                                       DB 1; Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 119;
                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (PRA-CH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X82010; CAA57537.1; -.
InterPro; IPR002496; PRA-CH.
Pfam; PF01502; PRA-CH; 1.
ProDom; PD002610; PRA-CH; 1.
Histidine blosynthesis; Hydrolase.
SEQUENCE 119 AA; 13389 MW; 2682DFA9EC17B69F CRC64;
Ribosomal protein.
SEQUENCE 105 AA; 11835 MW; 6C68DB611ED7F620 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-binding protein HEXBP (Hexamer-binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE-96349112; PubMed-8760919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 AA.
                                                    Score 29; DB 1
Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29; DB 1; Pred. No. 16; 1; Mismatches
                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
                                                    80.6%;
ilarity 71.4%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 80.6
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 TSGHVOR 70
                                                                                                                                                          33 TKGHLSK 39
                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TSGHLSR 7
                                                                                                                                     1 TSGHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (
01-FEB-1995 (
15-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodobacter
                                                                                                                                                                                                                                                                           HIS3_RHOSH
Q53158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEXP_LEIMA
Q04832;
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PROSITE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
CNBP_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART
   RRITAR OCCUPANTA DE LA COMPANTA DEL COMPANTA DE LA COMPANTA DEL COMPANTA DE LA COMPANTA DEL COMPANTA DE LA COMPANTA DEL COMPANTA DE LA COMPANTA DEL COMPANTA DE LA COMPANTA DEL COMPANTA DE LA COMPANTA DE LA COMPANTA DEL COMPANTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                 Webb J.R., McMaster W.R.;
"Molecular cloning and expression of a Leishmania major gene encoding a single-stranded DNA-binding protein containing nine 'CCHC' zinc finger motifs.";
J. Blol. Chem. 268:13994-14002(1993)
-!- FUNCTION: BINDS TO SINGLE-STRANDED DNA LOCATED IN THE 5'
HEXANUCLEOTIDE REPEAT REGION OF THE L.MAJOR LEISHMANOLYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Liver;
MEDLINE-95203870; PubMed-7896269;
Warden C.H., Krisans S.K., Purcell-Huynh D., Leete L.M.,
Daluiski A., Diep A., Taylor B.A., Lusis A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1D33892EF9F743D8 CRC64;
                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: CONTAINS 9 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 34, Last sequence update)
Cellular nucleic acid binding protein (CNBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCHC-TYPE 4.
CCHC-TYPE 5.
CCHC-TYPE 6.
CCHC-TYPE 7.
CCHC-TYPE 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                               STRAIN=NIH S;
MEDLINE-93300785; PubMed-8314766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28225 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 SGHMSR 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 AA;
                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGHLSR 7
Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNBP_MOUSE
P53996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                     family identified by genetic mapping and sequencing.";
Genomics 24:14-19(1994).
-!- FUNCTION: SINGLE STRANDED DNA-BINDING PROTEIN, WITH SPECIFICITY TO
-THE STEROL REGULATORY ELEMENT (SRE). CNBP IS INVOLVED IN STEROL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC-finger; DNA-binding; Transcription regulation; Repressor; Repeat.
ZN_FING 45 CCHC-TYPE 2.
ZN_FING 65 CCHC-TYPE 2.
ZN_FING 69 106 CCHC-TYPE 3.
ZN_FING 110 127 CCHC-TYPE 6.
ZN_FING 128 145 CCHC-TYPE 6.
ZN_FING 128 145 CCHC-TYPE 6.
ZN_FING 128 145 CCHC-TYPE 7.
VARIANT 2 2 S -> R (IN CLONE 6).
VARIANT 65 65 D -> DE (IN CLONE 14).
VARIANT 98 98 G -> D (IN CLONE 14).
SEQUENCE 170 AA; 18742 MW; 152BEC42881358E8 CRC64;
                                                                                                                                                                                   -i- TISSUE SPECIFICITY: PRESENT IN ALL TISSUES EXAMINED.
-i- SIMILARITY: TO S.POMBE BYR3 AND TO RETROVIRAL NUCLEIC ACID BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                        -!- SUBCELLULAR LOCATION: CYTOPLASMIC, ALSO PRESENT IN ENDOPLASMIC
"Mouse cellular nucleic acid binding proteins: a highly conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28; DB 1; Length 170; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                          -1- SIMILARITY: CONTAINS 7 CCHC-TYPE ZINC FINGERS.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 39;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:88431; Cnbp.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSS0159; C2HCZNFINGER.
400343; ZnF_C2HC; 7.
PSS0158; ZF_CCHC; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L12693; AAA89198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 211870; CAA77896.1; --
EMBL; X63866; CAA45345.1; --
EMBL; 211871; CAA77897.1; --
EMBL; U20326; AAB60490.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.8
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                               MEDIATED REPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 SGHLAR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 PROTEINS (NBP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00343;
                                                                                                                                                                RETICULUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNBP_CHICK
O42395;
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                                                                                                                                                                                                                                                                                                                                               EMBL; AF004942:

EMBL; AF004942:

InterPro; IPR001878; Znf_CCHC.

Pfam; PF00098; zf-CCHC; 7.

PRINTS; PR00939; C2HCZMFINGER.

SWART; SW00443; Znf_CCHC; 7.

PROSITE; PS50158; ZF_CCHC; 7.

Zhnc-finger; DNA-binding; Transcription regulation; Repressor; Repeat.

ZN_FING 4 21 CCHC-TYPE 1.

ZN_FING 46 63 CCHC-TYPE 2.
                    COMP. Biochem. Physiol. 118B:659-665(1997).

-! FUNCTION: SINGLE STRANDED DNA-BINDING PROFEIN, WITH SPECIFICITY TO THE STEROL REGULATORY ELEMENT (SRE). CNBP IS INVOLVED IN STEROL-MEDIATED REPRESSION (BY SIMILARITY).

-! SUBCELLULAR LOCATION: CYTOPLASMIC, ALSO PRESENT IN ENDOPLASMIC RETICCULUM (BY SIMILARITY).

-! SIMILARITY: TO S.POMBE BYR3 AND TO RETROVIRAL NUCLEIC ACID BINDING PROFEINS (NBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
"Sequence and tissue distribution of chicken cellular nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.8%; Score 28; DB 1; Length 172; 83.3%; Pred. No. 40; 1: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123F4E248A980390 CRC64;
                                                                                                                                                                               -!- SIMILARITY: CONTAINS 7 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCHC-TYPE 3.
CCHC-TYPE 4.
CCHC-TYPE 5.
CCHC-TYPE 6.
CCHC-TYPE 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19043 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 77.8
Best Local Similarity 83.3
Matches 5; Conservative
               protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 1
151 1
172 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZN_FING
ZN_FING
               binding
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Search completed: July 15, 2003, 12:53:30 Job time: 7.66667 secs

2 SGHLSR 7 ||||:| 159 SGHLAR 164

qq

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

- protein search, using sw model OM protein July 15, 2003, 12:50:51; Search time 12.3333 Seconds Run on:

(without alignments) 54.563 Million cell updates/sec

US-10-006-069A-247 36 1 TSGHLSR 7

Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

hypothetical prote hexamer-binding pr protein M01D1.1 [i probable cysteine hypothetical prote hypothetical prote estrogen receptor hypothetical prote hypothetical prote probable membrane protein kinase hom probable malate de Na+/H+ antiporter Ras interactor RIN hypothetical prote vesicle transport hypothetical prote probable myb-relat protein F10A5.22 [hypothetical prote protein F56B3.8 [1 i7 protein - vacci I7L protein - vacc topoisomerase II hypothetical prote hypothetical prote probable finger pr hypothetical prote phosphoribosyl-AMP Description B86128 T48965 S49467 40349 \$ Query Match Length DB Score Result Š

hypothetical coile sensory transducti	hypothetical prote hypothetical prote	hypothetical prote probable requiator	hypothetical prote hypothetical prote	hypothetical prote	hypothetical prote	calcimedin, 32K -	cellular nucleic a	zinc ringer protei cellular nucleic a
1.0		~ #	7 8	0 66	. on u	n 0	_	J 60
T50401 H69145	E96674	T23617	D61547 A95102	354593	T33669	309020	148297	A55499 I48298
2 2	77	77	~ ~	70	900	7 N	0	2 2
533	876 957	1696 87	87 111	111	153	157	170	171
80.6 80.6	80.6 80.6	80.6	77.8	77.8	77.8	77.8	77.8	77.8
29	5 7 7 8	28 28	78 78 78 78	. 28	989	78 78 78	28	78 78 78
30	33 33	34 35	36 37	38	0.4	4 4 7 7	43	4 4 5 5

ALIGNMENTS

(Saccharomyces cerevisiae) YBR0616 9-Sep-1994 #text_change 19-Apr-2002 se, C.; Vetter, I. se, August 1994	Piravandi, E.	; Length 220;	s cerevisiae)
	igust 1994	0; Indels 0; Gaps 0;	#text_change 19-Apr-2002
YBR066c - yeast thetical protein s cerevisiae quence_revision 0 5926 pt, G.; Schwarzlo n Sequence Databa	A; Wolecule type: DNBA A; Residues: 1-187 <fela \$288c="" \$45206="" \$45816="" \$6d:s0000270="" 124-220="" 235935;="" 2r="" 2r<="" <dom="" a;="" accession:="" august="" b.;="" c;="" cross-references:="" database,="" dna="" dondey,="" embl:="" experimental="" gassenhuber,="" genetics:="" grass-references:="" h.;="" map="" mips:ybr066c="" molecule="" number:="" obermaier,="" pirav="" position:="" protein="" r;="" reference="" residues:="" sequence="" source:="" strain="" submitted="" td="" the="" to="" type:=""><td>A; Note: YBR066c C; Keywords: nucleus; zinc finger C; Keywords: nucleus; zinc finger F;155-175/Region: zinc finger F;183-205/Region: zinc finger Ouery Match Best Local Similarity 100.0%; Pred. No. 1.9; Matches 7; Conservative 0; Mismatches Oy 1 TSGHLSR 7 Db 164 TSGHLSR 170</td><td>RESULT 2 S55078 hypothetical protein YDR043c - yeast (Saccharomyces NyAlternate names: hypothetical protein YD5112.01c C; Species: Saccharomyces cerevisiae C; Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #C; Accession: S55078 R; Oliver, K.; Harris, D. R; Oliver to the EMBL Data Library, June 1995 A; Reference number: S55078</td></fela>	A; Note: YBR066c C; Keywords: nucleus; zinc finger C; Keywords: nucleus; zinc finger F;155-175/Region: zinc finger F;183-205/Region: zinc finger Ouery Match Best Local Similarity 100.0%; Pred. No. 1.9; Matches 7; Conservative 0; Mismatches Oy 1 TSGHLSR 7 Db 164 TSGHLSR 170	RESULT 2 S55078 hypothetical protein YDR043c - yeast (Saccharomyces NyAlternate names: hypothetical protein YD5112.01c C; Species: Saccharomyces cerevisiae C; Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #C; Accession: S55078 R; Oliver, K.; Harris, D. R; Oliver to the EMBL Data Library, June 1995 A; Reference number: S55078

Sp

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Query Match 88.9
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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A; Residues: 1-265 <STO>
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A;Molecule type: DNA
A;Residues: 1-231 <OLI>
A;Cross-references: EMBL:Z49812; NID:g1204147; PID:g854427; GSPDB:GN00004; MIPS:YDR043c
A;Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40349
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
Submitted to the EMBL Data Library, March 1997
A;Reference number: 221922
A;Accession: T40349
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-214 < WOOD
A;Experimental source: strain 972h-; cosmid c389
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R; Yoshloka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: 217323; MUID:98162722; PMID:9501991
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A;Residues: 1-214 <YOS>
A;Cross-references: EMBL:D89116; NID:g1749439; PIDN:BAA13778.1; PID:g1749440
A;Experimental source: strain PR745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                 Score 33; DB 2; Length 231; Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 214;
15;
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Pred. No. 15;
0; Mismatches
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Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                         1; Mismatches
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A; Introns: 9/2; 44/3; 81/3; 165/3; 186/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.9%;
85.7%;
                                                                                  C;Genetics:
A;Gene: SGD:NKG1; MIPS:YDR043c
A;Cross-references: SGD:S0002450
A;Map position: 4R
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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185 TSGHLAR 191
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169 TSGHLDR 175
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probable myb-related DNA-binding protein [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C; Accession: G85016
R; Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp Nature 402, 769-777, 1999
A; Title: Sequence and annalysis of chromosome 4 of the plant Arabidopsis thaliana.
A; Accession: G85016
A; Accession: G85016
A; Setains preliminary
A; Molecule type: DNA
A; Residues: 1-285 <STO>
A; Cenetics:
C; Genetics:
A; Gene: AT4g01280
A; Gene: AT4g01280
A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein F10A5.22 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: D: Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: H96785
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alogn Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Mature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A; Authors: Hunter, J.L.; Jenkins, J.S.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: H96785
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C;Species: Caenorhabditis elegans
C;Species: L3-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T19449
R;Ainscough, R.
Submitted to the EMBL Data Library, October 1996
A;Reference number: 219125
A;Reference number: 219125
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Pred. No. 31;
2; Mismatches 0; Indels
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Pred. No. 20;
0; Mismatches
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Page

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RESULT 12
C84678
hypothetical protein At2g27900 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Genetics:
A;Gene: I7
C;Superfamily: vaccinia virus I7 protein
C;Keywords: late protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 86.1
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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74 SGHLSR 79
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74 SGHLSR 79
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A;Molecule type: DNA
A;Refathi, Z.; Condit, R.C.
A;Title: Genetic and molecular biological characterization of a vaccinia virus temperatu
A;Title: Genetic and molecular biological pMID:1994576
A;Accession: A38497
A;Refathe: Canda (A)
A;Refat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein FS6B3.8 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: A88633
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
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C; Species: vaccinia virus
C; Obate: 30-Jun-1999 sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C; Accession: G29889; A38497
R; Schmitt, J.F.C.; Stunnenberg, H.G.
R; Schmitt, J.F.C.; Stunnenberg, H.G.
A; Virol. 62, 1889-1889; J988
A; Title: Sequence and transcriptional analysis of the vaccinia virus HindIII I fragment.
A; Reference number: A29889; MUID: 88215015; PMID: 2835495
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                                                                  A Residues: 1-286 <WIL>
A; Residues: 1-286 <WIL>
A; Cross-references: EMBL: 281039; PIDN: CAB02773.1; GSPDB: GN00023; CESP: C25D7.2
A; Experimental source: clone C25D7
C; Genetics: A; Gene: CESP: C25D7.2
A; Gene: CESP: C25D7.2
A; Map position: 5
A; Map position: 5
A; Introns: 28/3; 128/3; 212/3
C; Superfamily: Caenorhabditis elegans hypothetical protein F36D3.4
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   A;Status: preliminary; translated from GB/EMBL/DDBJ
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100.0%; Pred. No. 33;
11ve 0; Mismatches
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Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conserv
                                           Molecule type: DNA Residues: 1-286 <WIL>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-357 <STO>
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A;Gene: F56B3.8
A;Map position: 4
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C;Accession: T37344
R;Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A;Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) st
A;Reference number: 220877
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                                                                                                                                                                                                                                                                               C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 08-Apr-1994
C;Accession: C42511
Submitted to GenBank, June 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: vaccinia virus
A;Variety: strain Ankara
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C;Accession: T37344
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-423 <ANT>
A, Cross-references: EMBL:094848; PIDN:AAB96439.1
A, Experintal source: strain Ankara
C, Genetics:
Score 31; DB 1;
Pred. No. 51;
0; Mismatches
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100.0%; Pred. No. 51;
iive 0; Mismatches
                                                                                                                                                                                                                                                                17L protein - vaccinia virus (strain Copenhagen)
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A; Reference number: A33172
A; Accession: C42511
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-423 <-0.50H>
C; Superfamily: vaccinia virus I7 protein
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C; Superfamily: vaccinia virus I7 protein
  Query Match 86.1%; Scc
Best Local Similarity 100.0%; Pi
Matches 6; Conservative 0;
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Search completed: July 15, 2003, 12:55:32
Job time : 14.3333 secs
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Best Local Similarity 100.0
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417 SGHLSR 422
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   K;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MuID:20083487; PMID:10617197
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C. Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C. Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C. Accessation: D7016
R. Kunst, F.: Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A. Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Roetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurlick, K.; Lapidus, A.; Ladinois,
A. Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
R. M.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A. Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toganoi, A.; Yasaumoto, K.; Yasumoto, Yasumoto, K.; Yasumoto, Yasumoto, K.; Yasumoto, 
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R; Maruyama, K.; Endoh, H.; Sasaki-Iwaoka, H.; Kanou, H.; Shimaya, E.; Hashimoto, S.; Kat Biochem. Blophys. Res. Commun. 246, 142-147, 1998
A; Title: A novel isoform of rat estrogen receptor beta with 18 amino acid insertion in the Reference number: JW0046; MUID: 98262932; PMID: 9600083
A; Accession: JW0046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: ERbeta2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Mar-1999
02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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100.0%; Pred. No. v...
0; Mismatches
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100.0%; Pred. No. 62;
1ve 0; Mismatches
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A;Residues: 1-503 <MAR>
A;Cross-references: DDBJ:AB012721
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Best Local Similarity 100.،
د.مه 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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A;Molecule type: DNA
A;Residues: 1-496 <STO>
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37 TSGHLS 42
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A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Recession: D70016
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Rosidues: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-531 < RUN>
A:Cross-references: GB:Z99120; GB:AL009126; NID:92635613; PIDN:CAB15232.1; PID:ell843
A:Reperimental source: strain 168
C;Genetics:
A:Genetics:
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R; BuchTrieser, C.; Rusniok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; Carn
Submitted to the EMBL Data Library, October 1998
A; Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
A; Reference number: 224348
A; Accession: T470017
A; Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
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66;
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81;
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A; Residues: 1-639 <BUC>
X, Cross-references: EMBL:AL031866; PIDN:CAA21360.1
A; Experimental source: strain 6/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein [imported] - Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.1%; Score 31; DB 100.0%; Pred. No. 81; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                               Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                               86.1%;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

; Search time 10.6667 Seconds July 15, 2003, 12:51:16 Run on:

(without alignments)
19.309 Million cell updates/sec

US-10-006-069A-68 36 1 RSDHLSR 7 Title: Perfect score:

Sednence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 262574 seqs, 29422922 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 69, Appl	94	96	3, A	'n	Sequence 6, Appli	7,	7,	Sequence 8, Appli	6	0	10,	73,	Sequence 116, App	112,	2, Ar	4	10	6, 1	12,	7,7	7	7	4	Sequence 16, Appl	Sequence 4, Appli	4
ID	US-09-173-941-69	US-09-229-007A-94	US-09-229-007A-96	US-08-620-151-3	US-08-570-227A-5	US-08-570-227A-6	US-08-570-227A-7	US-09-077-991-7	US-09-077-991-8	US-09-077-991-9	US-09-229-007A-9	US-09-229-007A-10	US-08-353-476-73	US-08-353-476-116	US-08-353-476-112	US-08-399-561-2	US-08-570-227A-4	US-08-570-227A-10	US-09-077-991-6	US-09-077-991-12	492-	US-08-570-227A-2	US-09-077-991-2	US-08-203-532F-4	US-08-950-860-16	US-09-078-465-4	PCT-US95-01882A-4
BB	4	4	4	7	~	N	7	4	4	4	4	4	N	~	~	Н	7	7	4	4	4	a	4	~	က	4	Ŋ
% Query Match Length DB	7	21	21	76	77	77	77	77	77	77	94	86	168	241	273	411	77	77	77	77	288	480	480	302	302	302	302
& Query Match	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	86.1	83.3	83.3	83.3	83.3	83.3	83.3	83.3	90.6	90.6	90.6	90.6
Score	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	31	30	30	30	30	30	30	30	59	53	29	53
Result No.	1	7	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

28	29		303	7	US-08-203-532F-2	Sequence 2, Appli
56	29	•	303	4	US-09-078-465-2	Sequence 2, Appli
30	29		303	S	PCT-US95-01882A-2	Sequence 2, Appli
31	59		299	7	US-08-718-661-2	7
32	28		7	4	US-09-173-941-71	71,
33	28	•	10	٣	US-09-139-762A-19	19,
34	28	77.8	10	٣	US-09-139-762A-53	53,
35	78	•	20	٦	US-08-040-548-19	19,
36	28		20	Н	US-08-466-344-19	_
37	78	•	21	4	US-09-229-007A-95	95,
38	28		24	4	US-08-874-569B-16	16,
39	28	•	26	7	US-08-620-151-111	111,
40	28		28	Н	US-08-040-548-34	34, 7
41	58		28	٦	US-08-466-344-34	34,
42	78	•	28	4	US-09-058-459-1	1, A
43	28		28	4	US-09-127-926-1	1,
44	28		28	4	US-09-037-179B-15	15,
45	28		28	4	US-09-240-179-2	Sequence 2, Appli
					ALIGNMENTS	
necma 1						
1 10000						

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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: nucleotide
COTHER INFORMATION: codon binding sequence
US-09-173-941-69
                         Sequence 69, Application US/09173941

Patent No. 6140081

GENERAL INFORMATION:
TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
FILE REFERENCE: NOV0081S

CURRENT APPLICATION NUMBER: GE_09/173,941

CURRENT FILING DATE: [1998-10-16]

NUMBER OF SEQ ID NOS: IZU

SEQ ID NO 69

LENGTH: 7
                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
RESULT 1
US-09-173-941-69
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Gaps ö Score 33; DB 4; Length 7; Pred. No. 2e+05; 0; Indels Mismatches Query Match 91.7%; Best Local Similarity 85.7%; Matches 6; Conservative

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1 RSDHLSR οy g

Sequence 94, Application US/09229007A Patent No. 6453242 US-09-229-007A-94

| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Elsenberg, Stephen P. |
| APPLICANT: Case, Casey C. |
| APPLICANT: Case, Casey C. |
| APPLICANT: Case, Casey C. |
| APPLICANT: Case Casey C. |
| APPLICANT: Case Casey C. |
| APPLICANT: Sandamo Blosciences, Inc. |
| APPLICANT: Sandamo Blosciences, Inc. |
| APPLICANT: Sandamo Blosciences, Inc. |
| TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins |
| TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins |
| TITLE OF INVENTION: OB Bind to Preselected Sites |
| FILE REFERENCE: 019496-001800US |
| FILE REFERENCE: 019496-00180US |
| CURRENT APPLICATION NUMBER: US/09/229,007A |
| SOFTWARE: PatentIn Ver. 2.1 |
| SEQ ID NO 94

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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||||
13 RSDHLSK 19
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RSDHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-570-227A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Designing Zinc Finger Proteins
                                                                                                                                                                                                                                                                                                                                                          US-09-229-007A-96

Sequence 96, Application US/09229007A

Sequence 96, Application US/09229007A

Sequence 96, Application US/09229007A

Sequence 96, Application US/09229007A

Sequence 10. 66.53242

GENERAL INFORMATION:

APPLICANT: Easenberg, Stephen P.

APPLICANT: Casey C.

APPLICANT: Gasey C.

APPLICANT: Sangame Blosciences, Inc.

APPLICANT: Sangame Blosciences, Inc.

APPLICANT: Separ, Edward J.

APPLICANT: Sangame Blosciences, Inc.

TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins TITLE OF INVENTION: Disciple 001800US

CURRENT FILING DATE: 1999-01-12

CURRENT FILING DATE: 1999-01-12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 96

LENGTH. 21

PLENGTH. 21
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: 2FP sequence; OTHER INFORMATION: (F1, F2 and F3) from SBS design GR-223 US-09-229-007A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence
; OTHER INFORMATION: (F1, F2, F3) from SP1
US-09-229-007A-96
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APPLICANT: Imperiall, Barbara
APPLICANT: Imperiall, Grant K.
APPLICANT: Walkup, Grant K.
TITLE OF INVENTION: DEPTIDYL FLUORESCENT CHEMOSENSOR FOR
TITLE OF INVENTION: DIVALENT ZINC
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: BRINKS, HOFER, GILSON & LIONE
                                                                                                                                                                      Score 33; DB 4; Length 21;
Pred. No. 0.95;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 4; Length 21; Pred. No. 0.95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08620151
Patent No. 5928955
                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                        91.7%;
85.7%;
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.7%
                                                                                                                                                                      Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60611-5599
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                   15 RSDHLSK 21
                                                                                                                                                                                                                                                             1 RSDHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-620-151-3
LENGTH: 21
                                                                  FEATURE:
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Gaps
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APPLICANT: Spelsberg, T. C.
TITLE OF INVENTION: DNA ENCONDING TGF-BETA INDUCIBLE
TITLE OF INVENTION: EARLY FACTOR-1 (TIEF-1), A GENE EXPRESSED
TITLE OF INVENTION: BY OSTEOBLASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
ZIP: 55402
MOUTEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 26;
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,151
FILING DATE: 22-MAR-1996
CLASSIFICATION: 42.2
ATTORNEY/AGENT INFORMATION:
NAME: Shannon, Karen L.
REGISTRATION NUMBER: 36,675
REFERENCE/DOCKET NUMBER: 8597/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FASTEM: DOS SOFTWARE: FASTESED Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/570,227A FILING DATE: 11-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08570227A Patent No. 5981217 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Woessner, Warren D
REGISTRATION UDMBER: 30,440
REFERENCE/DOCKET WUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: TRNGTH: 26 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.7-
انگریم 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-620-151-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 612-359-3263
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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91.78;
85.78;
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SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 91.7
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                   55402
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   US-08-570-227A-7
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US-09-077-991-7
                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                       CITY: N
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
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0
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A. STREET: P.O. Box 2938
CITY: Minneapolis
                                                                                                         Score 33; DB 2; Length 77;
Pred. No. 3.8;
                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 77
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                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Subramaniam, M.
APPLICANT: Spelsberg, T. C.
TITLE OF INVENTION: DNA ENCONDING TGF-BETA INDUCIBLE
TITLE OF INVENTION: EARLY FACTOR-1 (TIEF-1), A GENE FITTE OF INVENTION: BY OSTEOBLASTS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY /***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 150.157US1
TELECOMMUNICATION:
TELEPHONE: 612-359-3260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDLIN TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATE:
APPLICATION NUMBER:
ELLING DATE: 11-DEC-1995
                                                                                                                                                                                                                                                                              Sequence 6, Application US/08570227A Patent No. 5981217
                                                                                                         91.7%;
85.7%;
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.73
Matches 6; Conservative
LENGTH: 77 amino acids
                                                                                                                                        6; Conservative
                             STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 612-359-32 TELEFAX: 612-359-3263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111111:
70 RSDHLSK 76
                                                                                                                                                                                          111111:
70 RSDHLSK 76
                                                                                                                         Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                     1 RSDHLSR 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MN
                                                                                                                                                                                                                                                              US-08-570-227A-6
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                                                                            US-08-570-227A-5
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                                                                                                           Query Match
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Gaps
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APPLICANT: Subramaniam, M.
APPLICANT: Subramaniam, M.
APPLICANT: Subramaniam, M.
APPLICANT: Sublaberg, T.C.
APPLICANT: Rocche, P.C.
TITLE OF INVENTION: TGF-Beta inducible early factor-1
TITLE OF INVENTION: (TIEF-1) and a method to detect breast cancer:
FILE REFERENCE: 150.1570S2
CURRENT APPLICATION NUMBER: US/09/077,991
CURRENT FILING DATE: 1998-07-07
EARLIER APLICATION NUMBER: PCZ/US96/19555
FARLIER FILING DATE: 1995-12-11
EARLIER FILING DATE: 1995-12-11
Sequence 7, Application US/08570227A
Patent No. 5981217
GENERAL INFORMATION:
APPLICANT: Subramaniam, M.
APPLICANT: Spelsberg, T. C.
TITLE OF INVENTION: BARLY FACTOR-1 (TIEF-1), A GENE EXPRESSED TITLE OF INVENTION: BY OSTEOBLASTS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                               ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A. STREET: P.O. Box 2938 CITY: Minneapolis
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Pred. No. 3.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,227A
FILING DAFE: 11-DEC-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150.157US1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: WGESENEY, WARTEN D
REGISTRATION NUMBER: 30.440
REFERENCE/DOCKET NUMBER: 150.
TELECOMUNICATION INFORMATION:
TELEPHONE: 612-359-3263
TELEPAX: 612-359-3263
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RESULT 7

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1; Mismatches
                                                         Score 33;
Pred. No.
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                      91.7%;
85.7%;
                                                         Query Match 91.7
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                  10 RSDHLSK 76
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                                                                                                                                                                 1 RSDHLSR 7
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                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          US-09-229-007A-9
        US-09-077-991-9
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LENGTH: 94
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Sequence 9, Application US/09077991
Retent No. 6207375
GENERAL INFORMATION:
APPLICANT: Subramaniam, M.
APPLICANT: Spelsberg, T.C.
TITLE OF INVENTION: TGF-Beta inducible early factor-1
TITLE FA
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                                                                                                                                                                                                                                             Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 7
                                                                                                                                                                                       91.7%;
85.7%;
                                                                                                                                                                                    Query Match 91.7
Best Local Similarity 85.7
Matches 6; Conservative
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                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-077-991-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Matches 6; Conser
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..rrLICANT: Case, Casey C.

APPLICANT: Case, Casey C.
APPLICANT: Case, Casey C.
APPLICANT: Jamieson, Andrew
APPLICANT: Jamieson, Andrew
APPLICANT: Sengamo Biosciences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Lases
TITLE NEFERENCE: 019496-001800US
CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1999-01-12
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
TYPF.
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                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Elsenberg, Stephen P.
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Case, Casey C.
APPLICANT: Cox III, George N.
APPLICANT: Cox III, George N.
APPLICANT: Sengamon, Andrew
APPLICANT: Rebar, Edward J.
APPLICANT: Sengamon Blosclences, Inc.
APPLICANT: Sengamon Blosclences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger Proteins
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: to Bind to Preselected Sites
CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1999-01-12
SUPPRENT FILING DATE: 1999-01-12
SUPPRENT FILING DATE: 2.1
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                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%; Score 33; DB 4; Length 94;
85.7%; Pred. No. 4.7;
ive 1; Mismatches 0; Indels
Length 77;
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                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Weininger, Arthur M
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
SADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st St., Suite A-1
CITY: Galnesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 168;
; OTHER INFORMATION: transcription factor consensus sequence US-09-229-007A-10
                                                     Length 98;
                                                                                        0; Indels
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Patent No. 5871902
GENERAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOUTHWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/353,476 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                     Score 33; DB
Pred. No. 4.9;
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                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              Sequence 73, Application US/08353476
Patent No. 5871902
                                                 91.7%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 168 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                    Query Match
Best Local Similarity 85.7-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.7
Best Local Similarity 85.7
Matches 6; Conservative
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80 RSDHLSK 86
                                                                                                                       1 RSDHLSR 7
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US-08-353-476-116
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                                                                                                                                                                                                             RESULT 13
US-08-353-476-73
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 112, Application US/08353476
Patent No. 5871902
GENDRAL INFORMATION:
APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WIT
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
  SPECIFIC SEQUENCE COMPOSITION
                                                                                                                                                             ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
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TITLE OF INVENTION: SPECIFIC SEQUENCE C NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS: ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: BENCEN, Gerard: 35,746
REFERENCE/DOCKET NUMBER: 37,746
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 375-800
INFORMATION FOR SEQ ID NO: 116:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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85.7%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                     Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RSDHLSR 7
                                                                                                                      STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32606
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US-08-353-476-112
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Search completed: July 15, 2003, 12:56:09 Job time: 11.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 15, 2003, 12:50:16; Search time 23.6667 Seconds (without alignments) 60.944 Million cell updates/sec Run on:

US-10-006-069A-68 36 1 RSDHLSR 7

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 segs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_virus:*
sp_archeriap:* SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_human:*
6: sp_mammal:* sp_mhc:* sp_organelle:* sp_phage:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q20766 caenorhabdi	P79289 sus scrofa	Q8uuu4 xenopus lae	Q95r58 drosophila	Q9wtq3 rattus norv	Q9vpq5 drosophila	Q8vi67 mus musculu	Q8tdd2 homo sapien	Q96mjl homo sapien	Q64167 mus musculu	Q90wr9 gallus gall	O89090 mus musculu	Q62445 mus musculu	Q63158 rattus norv	O89087 mus musculu	Q9vcb2 drosophila
	er er	020766	P79289	080004	Q95R58	Q9WTQ3	Q9VPQ5	08VI67	Q8TDD2	Q96MJ1	064167	Q90WR9	060680	062445	063158	089087	Q9VCB2
	DB	2	9	13	Ŋ	11	S	11	4	7	11	13	Ξ	11	11	Π	2
	Match Length DB	1363	237	278	347	415	426	428	431	452	467	760	781	782	783	784	968
æ :	Match	100.0	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7
	Score	36	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
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Q60488 cavia porce	Q8ruf4 oryza sativ	Q9vlx0 drosophila	Q9fj71 arabidopsis	005687 mycobacteri	Q9n492 caenorhabdi	Q9czy8 mus musculu	Q9cyl9 mus musculu	Q9crj0 mus musculu	Q9bhe3 leishmania	P91329 caenorhabdi	Q9sga2 arabidopsis	Q9w1w2 drosophila		046016 caenorhabdi	093567 gallus gall	O88939 mus musculu	09qz48 rattus norv	O95365 homo sapien	073453 homo sapien	Q8vcz7 mus musculu	Q9d9x5 mus musculu	001348 drosophila	Q9vtd3 drosophila	Q8tfx9 aspergillus	077251 drosophila	Q9dcc0 mus musculu	Q9uk33 homo sapien	Q9db38 mus musculu
11 060488	10 Q8RUF4	ONTXO	10 Q9FJ71	2 005687	5 Q9N492	11 Q9CZY8	11 Q9CYL9	11. Q9CRJ0	5 Q9BHE3	5 P91329	10 Q9SGA2	5 Q9W1W2	5 Q9TZ64	5 046016		11 088939		1 095365	1 073453	11 Q8VCZ7	11 Q9D9X5	5 001348	5 Q9VTD3	3 QSTFX9	5 077251	11 Q9DCC0	\$ Q9UK33	11 Q9DB38
1464	824	972	1332 1	86	168	195	204	212	300	309	361	410	497	543	546	565	569	584	619	619	746	750	. 801	1210	100	120	172	172
91.7	88.9	88.9	6.88	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	83.3	83.3	83.3	83.3
33	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	30	30	30	30
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	Gaps
PRELIMINARY; PRT; 1363 AA. -1998 (TrEMBLrel. 05, Created) -2001 (TrEMBLrel. 19, Last sequence update 2002 (TrEMBLrel. 21, Last annotation update 5 protein. -2002 (TrEMBLrel. 21, Last annotation update 2002 (TrEMBLrel. 21, Last annotation update 3 protein. -2002 (TrEMBLrel. 21, Last sequence update 5 protein. -2002 (TrEMBLrel. 21, Last annotation update 3 protein. -2002 (TrEMBLrel. 21, Last annotation update 3 protein. -2002 (TrEMBLrel. 21) -2006 (Jul. 1996) to the EMBL/GenBank/DDBJ date N. A. -2006 (Jul. 1996) to the EMBL/GenBank/DDBJ date 3 protein and biology. " -2007 (TrEMBLRel. 21) -2007 (TrEMBRel. 21) -2007 (TrEMBRel. 21) -2007 (TrEMBRel. 21) -2007 (TrEMBRel. 2	Ouery Match 100.0%; Score 36; DB 5; Length 1363; Best Local Similarity 100.0%; Pred. No. 29; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
RESULT 1 020766 DD 020766; DT 01-JAN-1 DT 01-DEC-2 DT 01-JUN-2 DE F54D1.5. GN F64D1.5. GN F64D1.5. GN CAMPAINTON CN CAMPAINTON COMPAINTON COMPAIN	Query Match Best Local Matches
KOH 4 D D D D D O O O K K K K K K K K K K K K	

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DB 13; Length 278;
                                                                                                                                           347 AA
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                                    1; Mismatches
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              Score 33;
                          Pred. No
                                                                                                                                                                  Created)
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                       Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 91.7
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                           PRELIMINARY;
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                                                                         111111:
249 RSDHLSK 255
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253 RSDHLSK 259
                                                          1 RSDHLSR 7
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uchida S.;
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              Query Match
                                                                                                                                           095R58
                                                                                                                                                        095R58
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                                                                                                                    RESULT 4
Q95R58
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Q9WTQ3
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                                                                                                                                                                                                            "Expression and regulatory function of the transcription factor Spl in the uterine endometrium at early pregnancy: implications for epithelial phenotype.";
MADI. Cell. Endocrinol. 159:159-170(2000).
EMBI. U57347; AAB39513.3; -.
HSSP: P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                             Spl transcription factor (Fragment).
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartlodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ossipova O., Stick R., Pieler T.; Interaction between two novel Spl-like zinc finger proteins and Brachyury in Xenopus.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AR062263; AAL47216.1; InterPro: IPR000822; Znf_C2H2. Pfam; PF00096; zf-C2H2.
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                                                                                                                                                                           MEDLINE-20150569; Pubmed-10687861;
Simmen R.C.M., Zhang X.L., Zhang D., Wang Y., Michel F.J.,
Simmen F.A.;
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85.7%; Pred. No. 21;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       25421 MW; C6950DB42912DAB6 CRC64;
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                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Spl-like zinc-finger protein XSPR-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0048; ZINCFINGER.

Prodom; PD000003; Znf_C2H2; 1.

SMART; SM00355; ZnF_C2H2; 3.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_3.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
                        237 AA.
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
DNA-binding; Metal-binding; Zinc-finger.
                                               Created)
                        PRT;
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ProDom; PD000003; znf_C2H2; 2.
SMART; SM00355; znF_C2H2; 3.
                                                                                                                                                                                                                                                                                nterPro; IPR000822; Znf_C2H2.
                                             01-MAY-1997 (TrEMBLrel. 03, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2002 (TrEMBLrel. 21,
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Best Local Similarity 85./*,
Best Local Similarity 65./*
                        PRELIMINARY;
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237 AA;
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TISSUE-ENDOMETRIUM;
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                                                                                                                               NCBI_TaxID=9823;
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SEQUENCE
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NON_TER
                       P79289
P79289;
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RESULT 2
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            P79289
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EP2237 OR CG4427.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebydroidea; Drosophilidae; Drosophila.
   Gaps
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNW-2002 (TrEMBLrel. 21, Last annotation update)
Kruppel-like transcription factor.
Rattus norvegicus (Rat).
Eattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ctapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EWBL/GenBank/DDBJ databases.
FNBL: AY061602; AAL291601: -
FlyBase; FBGH0043364; EB2237.
InterPro; IRR000822; Znf_C2H2.
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Indels
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO20759; BAA78378.1; --
HSSP; P08047; 1SP2.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; Zf_C2H2; 3.
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347 AA; 37832 MW; 153C660EEB49DFEF CRC64;
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Last annotation update)
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Prodom; PD000003; znf_CZHZ; 2.
PROSITE; PS00028; zINC_FINGER_CZHZ_1; UNKNOWN_3.
PROSITE; PS50157; zINC_FINGER_CZHZ_2; 3.
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Q8VI67;
Q8VI67;
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Q8VI67
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1D 08
AC 06
AC 01
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DT 01
DE 05
OC EU
CC MA
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RA Manatides P.G., Scherer S.E. Li P.W., Hoskins R.A., Calle R.F.,
George R.A., Lewis S.E., Hichards S., Ashburner M., Henderson S.N.,
Ramaratides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,
George R.A., Lewis S.E., Hichards S., Ashburner M., Henderson S.N.,
RA Bardon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Delcher A., Bouck J., Brokstein P., Brottier P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Buchtier P.,
RA Butris K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dalle C., Perriar C., Perriar S., Dietz S.M.,
Rodson K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
R. Burtis K.C., Gabrielian A.E., Garg N.S., Calbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorral C., Perraz C., Perriars S., Pleischmann W.,
RA Harris N.L., Harvey D., Heilman T.J., Hernadez J.R., Rednison J.A., Karatte S., Kulp D., Lai Z.,
Alalall M., Kalles F., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,
Ballako P., Lei Y., Levilsky A.A., Li J., Li J. Liang Y., Lin X.,
RA Milshina N.V. Mobarry C., Morris J., Mosherfi A.,
Rablook M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Rhout S.M., Moy W., Wurphy B., Wurphy J., Wary B., Sun E.,
Rhot R., Relact R., Span S., Pollatd J., Puri, Van R.,
Rhand B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith H.O.,
Rhen B.C., Siden Klamos I., Simpson M., Skupski M.P., Shon S., Yeologe T., Worley K., Wang S., Yao Q.A.,
R. Wang Z.-Y., Rassarman D.A., Weinster B., Schoeler F., Sprad D., Shon G., Stabelon W., Stupski M., Wang Z.-Y., Rassarman D.A., Weinster B., Stape G., Shon G., Stener S., Shon M., Stene
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                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neotera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                        Gaps
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                                                                                     Score 33; DB 11; Length 415;
Pred. No. 37;
1; Mismatches 0; Indels
SMART; SM00355; ZNE_C2H2; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 415 AA; 44147 MW; 9569CC3ACE98722F CRC64;
                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                         91.78;
85.78;
                                                                          Query Match
Best Local Similarity 85.7-
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391 RSDHLSK 397
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EP2237 OR CG4427.
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The Novel zinc Finger-Containing Transcription Factor Osterix is sequired for Osterblast Differentiation and Bone Formation."; Cell 108:17-29(2002). EMBL: AF184902; AAL60067.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manumalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
[1]
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                                                                                                                                                                                                                            Length 426;
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InterPro; IPR000822; Znf_C2H2.
Ffam; PP00096; ZirC2H2; 3.
PRINTS; PR000048; Znf_C2H2; 1.
PRODOM; PD0000048; Znf_C2H2; 1.
PROSITE; PS00028; Znr_CZH2; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_1; GNKNOWN_3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
SEQUENCE 428 AA; 44718 MW; B794988958743586 CRC64;
FlyBase; FBGN0043364; EP2237.
InterPro; IPR000822; Znf_C2H2.
Promo, PP00096; Zf_C2H2; 3.
Promo, PR000003; Znf_C2H2; 2.
SMART; SM00355; ZnF_C2H2; 3.
PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 426 Aa, 46491 MW; 7D3626F2C2CAOAE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
0sterix.
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                                                                                                                                                                                                                         Score 33; DB 5
Pred. No. 38;
1; Mismatches
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                                                                                                                                                                                                                         91.7%;
85.7%;
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                                                                                                                                                                                                  Ouery Match
Best Local Similarity 85./v
6; Conservative
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                                                                                                                                                                                                                                                                                                                                            332 RSDHLSK 338
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                  1 RSDHLSR 7
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111111:
381 RSDHLSK 387
                                                                                      SEQUENCE FROM N.A.
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SEQUENCE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q90WR9
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ32295 fis, clone PROST2001823, weakly similar to transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Watanabe M., Fulimori K., Tanai H., Ishida M., Yamashita H., Chiba Y., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishil S., Yamamorco J., Isono Y., Kawat Hio Y., Satio K., Nishikawa T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Nishikawa T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, RAO56857; BAB71297.1; -.
InterPro: IPR000822; Znf_CZH2.
                                                                                                                                                                                                                                        Gaps
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Trans-acting transcription factor 1 (Transcription factor SP1) (SP1
                                     Ganss B.W.; "cDNA sequence, gene structure and chromosomal localization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                            4; Length 431;
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Pred. No. 41;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                        Indels
                                                                             human osterix (OSX) gene.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF477981; AAL84281.1; -.
SEQUENCE 431 AA; 44994 MW; 454A6FEA84309FF9 CRC64;
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
DNA-DIAding; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                           452 AA.
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                                                                                                                                                                                         Score 33; DB
Pred. No. 39;
1; Mismatches
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Similarity 85.7%;
6; Conservative
                                                                                                                                                                                                                                      6; Conservative
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SEQUENCE FROM N.A.
TISSUE-OSTEOSARCOMA;
                                                                                                                                                                                                                                                                                                 111111:
365 RSDHLSK 371
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389 RSDHLSK 395
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Best Local Similarity
                                                                                                                                                                                                                                                                             1 RSDHLSR 7
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Best Local Similarity
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SP1.
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Matches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_raxID=10090;
                                                                                                                                             MEDLINE-96016118; PubMed-7568082;
Persenglev S.P., Saffer J.D., Kilpatrick D.L.;
An alternatively spliced form of the transcription factor Spl
containing only a single glutamine-rich transactivation domain.";
Proc. Natl. Acad. Sci. U.S.A. 92:9107-9111(1995).
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85.7%; Pred. No. 42;
1.ve 1; Mismatches 0; Indels
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PRINTS; PR00048; ZINCFINGER.
ProDom; D0000031; Znf_C2H2; 2.
SMART; SM00355; ZnF_C2H2; 3.
PROSITE; PS00128; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
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50 AA; 78561 MW; 4ECBBE9DB49A8594 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Transcription factor.
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Probom; PD000003; znf_C2H2; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:98372; Spl.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; S79832; AAB35321.1; --
EMBL; X60136; CAA42721.1; --
HSSP; P08047; 1SP1.
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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MGD; MGI:107595; Sp4.
InterPro; IPR008923; Znf_C2H2.
InterPro; Zf-C2H2; 3.
PRINTS; PR000048; ZINCFINGER.
PRINTS; PR000048; ZINC_FINGER.
SMART; SM00155; Znf_C2H2; 2.
SMART; SM00158; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
DNA-binding; Muclear procein; Zinc-finger.
SEQUENCE 782 AA; 81966 MM; 50BDA3DGC0848A4F CRC64;
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089087
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Q63158
       DDT REPRESENTATION OF THE PROPERTY OF THE PROP
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-!- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
TRANSFAC; T02414; -.
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                                                                                                                                                                                                                                                                                                 SP1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-NEUROBLASTOMA;
MEDILINE-98290554; PubMed-9628590;
Yajima S., Lee S.H., Minowa T., Mouradian M.M.;
"Sp family transcription factors regulate expression of rat D2
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Pred. No. 73;
1; Mismatches 0; Indels
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InterPro; IPR000822; Znf_CZH2.
InterPro; IPR000822; Znf_CZH2.
InterPro; IPR00084; Znf_CZH2.
IPRINTS; PR00048; ZINCFINGER.
SMART; SM00355; Znf_CZH2; 2.
PROSITE; PS00028; ZINC_FINGER_CZH2_1; 3.
PROSITE; PS0057; ZINC_FINGER_CZH2_2; 3.
DNA-binding; Metal-binding; Muclear protein; Zinc_finger.
SEQUENCE 781 AA; 80486 MW; 14CD12BBC58CF921 CRC64;
                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dopamine receptor gene.";
DNA Cell Biol. 17:471-479(1998).
EMBL; BYF062256; AAC16484.1;
HSSP; P08047; 1SP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.7%;
85.7%;
                                                                                                                                                                                                                                                                              Pranscription factor Spl.
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nes 6; Conservative
                                                                                                                                                             PRELIMINARY;
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                          111111:
670 RSDHLSK 676
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695 RSDHLSK 701
  RSDHLSR 7
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                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Q62445;
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Matches
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID*10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY; TISSUE-HEART;
MEDLINE-93309478; PubMed-8321243;
Zhu H., Nguyen V.T.B., Brown A.B., Pourhosseini A., Garcia A.V.,
van Bilsen M., Chien K.R.;
"A Novel, Tissue-Restricted Zinc Finger Protein (HF-1b) Binds to the
Cardiac Regulatory Element (HF-1b/MEF-2) in the Rat Myosin Light
Chain-2 Gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
Score 33; DB 11; Length 782;
Pred. No. 73;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%; Score 33; DB 11; Length 783;
85.7%; Pred. No. 73;
1.ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFC; T024,151.

TRANSFC; T024,515.

InterPro; IPR000822; Znf_C2H2.

Priam; PR00046; ZirC2H2; 3.

PROD00003; Znf_C2H2; 2.

SMART; SM00355; Znf_C2H2; 3.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.

DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.

SEQUENCE 783 AA; 81984 MW; 394AA6D4DEA5A197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; U07610; AAA17375.1; --
HSSP: P08047; 1SP1.
                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                  783 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Cell. Biol. 13:4432-4444(1993)
     91.7%;
85.7%;
                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21, Zinc finger protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 91.7
Best Local Similarity 85.7
Matches 6; Conservative
                                                      Conservative
                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                  ||||||||
|RSDHLSK 722
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  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                      1 RSDHLSR 7
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                                                                                                                                                               Mus musculus (Mouse).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_raxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 11; Length 784;
Pred. No. 73;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
SEQUENCE 784 AA; 80705 MW; F658BEF0A64E146A CRC64;
                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Transcription factor SP1.
 784 AA.
 PRT;
                                                                                                                                                                                                                                                                         fam; PF00096; zf-C2H2; 3.
PRINTS: PR00048; ZINCFINGER.
PRODOM: PD000003; Znf_C2H2; 2.
SMART; SM00355; ZnF_C2H2; 3.
                                                                                                                                                                                                                                                 MGD; MGI:98372; Spl.
InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                               91.7%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7
Matches 6; Conservative
. PRELIMINARY;
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| 698 RSDHLSK 704
                                                                                                                                                                                                                                                                                                                                                                                                                                1 RSDHLSR 7
                                                                                                                                          SEQUENCE FROM N.A.
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Search completed: July 15, 2003, 12:54:49 Job time: 25.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 15, 2003, 12:49:31; Search time 6.66667 Seconds (without alignments) 43.550 Million cell updates/sec Run on:

US-10-006-069A-68 36 1 RSDHLSR 7 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scription	Q9epw2 musculu	Q9uih9 homo sapien	drosc		P08047 homo sapien	rattu		Q55276 synechococc	_	Q13886 homo sapien	_	Q01713 rattus norv	P58334 mus musculu	Q9bxk1 homo sapien	면	-	mus	Q13118 homo sapien	008876 rattus norv	Q9epf4 mus musculu	рошо		_	Q08263 chlorobium	P39021 xenopus lae	P50222 homo sapien	P32443 mus musculu	P39020 rattus norv	Q9upg8 homo sapien	P53848 s folic aci	4	26633 cricetulu	P26634 dusicyon th
SUMMARIES	ΩI	KLFF_MOUSE	KLFF_HUMAN	BTD_DROME	SP4_HUMAN	SP1_HUMAN	SP1_RAT	KLF8_HUMAN	LCYB_SYNP7	SP6_MOUSE	BTE1_HUMAN	BTE1_MOUSE	BTE1_RAT	BTE4_MOUSE	BTE4_HUMAN	KLFD_HUMAN	KLFD_MOUSE	KLFA_MOUSE	KLFA_HUMAN	KLFA_RAT	KLFB_MOUSE	KLFB_HUMAN	SP2_HUMAN	SP3_HUMAN	YPPC_CHLLI	MOX2_XENLA	MOX2_HUMAN	MOX2_MOUSE	MOX2_RAT	PAL2_HUMAN	FAS_YEAST	EGR1_SERCA	EGR2_CRILO	EGR2_DUSTH
	DB	П	Н	Н	Н	Н	٦	-	-	-	-	П	-	Н	Н		Н	٦	П	-	7	-	Н	-	-	Н	7	Н	П	н	,	Н	Н,	-
	Length	415	416	644	784	785	788	359	411	152	244	244	244	251	252	288	289	479	480	480	511	512	909	711	203	298	303	303	303	496	864	29	62	62
æ	Query Match		91.7	91.7	91.7	91.7	91.7	86.1	ů.	83.3	۳.	æ.	æ.	83.3	€.	m	3	m	83.3	3	3	83.3	m	83.3	90.6	90.6	90.6	80.6	0	0	0	7	77.8	77.8
	Score	33	33	33	33	33	33	31	31	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	29	29	29	58	29	29	29	28	58	28
	Result No.	1	7	e CO	4	S	9	7	œ	σ,	10	11	12	13	14	. 15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

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34	28	77.		-	EGR2_POERE	P26635 poecilia re
35	28	77.1			I.VB2_BUNMU	P00989 bungarus mu
36	28	77.8	8 193	-	EGR1_POEGU	
37	28	77.1			EGR1_CHICK	073691 gallus gall
38	28	77.1		-	EGR1_COTJA	_
39	78	77.1			KTHY_HALN1	Q9hnv4 halobacteri
40	28	77.1		•	GDIR_BOVIN	P19803 bos taurus
41	78	77.		بر	EDAD_MOUSE	Q8vhx2 mus musculu
42	28	77.			EGL5_CAEEL	P17486 caenorhabdi
43	78	77.1			KLF6_HUMAN	Q99612 homo sapien
44	28	77.1		Т	KLF6_MOUSE	008584 mus musculu
4.5	28	77.1		_	KLF6_RAT	035819 rattus norv
					ALIGNMENTS	
RESULT 1						

	KLFF_MOUSE STANDARD; PRT; 415 AA.	Vorma; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Pel. 41, Tast commons undate)	15-JUN-2002 (Rel. 41, Last annotation update)	Krueppel-like factor 15 (Cardiovascular Kruppel-like factor). KIRTS OR CKIR	(Mouse)	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,			SEQUENCE FROM N.A. STRAIN-BALB/C:	S.J., Kuo C.T., Leiden J.M., Jain M.K.;	"CKLF, a cardiovascular Kruppel-like factor."; Submitted (Office 2000) to the most (Carbant Arthross	irthed (OCI-2000) to the imbalayeribalia/DDD databases.	SEQUENCE FROM N.A.	STRAIN-C57BL/6J; TISSUE-Tongue;		Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,	tawa I., Hara A., Fukunishi I., Konno H., Adachi J., Fukuda S.,	Arzawa n., izawa m., nishi n., niyosawa n., nondo s., iamanaka i., Saito T., Okazaki Y., Golobomi T., Bono H., Kasukawa T., Saito R.,	ota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		II P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J., المائية الله والمائية المائية ا		Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,	vnstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,	incich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,	LYONS F., MAICHIONNI L., MASJING J., MAZZAIELL J., MONDAELLS F., Nordone P., Ring R., Ringwald M., Rodrignez I., Sakamoto N.,	iki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch KF.,	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,	shaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,	Hayashisasi annotation of a full-length mouse only collection ".	585-690/2001)	. (+004)000 0000000000000000000000000000000	SEQUENCE FROM N.A.	TISSUE-Liver;	Strausberg R.;	nitted (SEP-2001) to the RMBL/GenBank/DDBJ databases.		DELONGS 10 10E SF1 FAMILI OF	
RESULT 1 KLFF_MOUSE	KLFF	15-JUN-	15-0	Krue	Mus	Euka	NCBL	[1]	SEQU	Gray	"CKL	[2]	SEQU	STRA	MEDL	Kawa	ALGK	Sait	Kado	Flei	Kuen	Saka	Blak	Brow	Gust	NO.C	Sasa	Suzu	Wyns	Haya	Na tan	[3]	SEQU	TISS	Stra	Subm		_	
RE Z	25	225	ដី	E C	SO	88	38	RN	8 P	8	Z i	N E	RP	RC	XX	RA 6	£ 6	\$ \$	RA	RA:	A G	2 Z	Æ	ΡĀ	8 8	¥ &	Æ	RA	8	¥ E	1 4	Z.	RP	2	RA	报	3 5	ខ្ល	ر

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TRANSFAC; T05058; -.
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BTD_DROME
                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                              ö
   and for commercial
                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELULIAR LOCATION: Nuclear.
TISSUE SPECIFICITY: Highly expressed in liver, followed by heart, skeletal muscle, and kidney. Not expressed in bone marrow or
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uchida S., Tanaka Y., Ito H., Saitoh-Ohara F., Inazawa J., Yokoyama K.K., Sasaki S., Marumo F., "Transcriptional regulation of the CLC-K1 promoter by myc-associated zinc finger protein and kidney-enriched Kruppel-like factor, a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Cell. Biol. 20:7319-7331(2000).
                                                                                                                                                                                             PROSITE; PSO0028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PSO157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; DNA-binding; Activator; Nuclear protein;
Transcription regulation; DNA-binding; Activator; Nuclear protein;
ZN FING 320 344 C2H2-TYPE.
ZN_FING 350 374 C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Krueppel-11ke factor 15 (Kidney-enriched kruppel-11ke factor).
                                                                                                                                                                                                                                                                                                                                              Score 33; DB 1; Length 415;
Pred. No. 5.3;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                              0; Indels
   Usage by
                                                                                                                                                                                                                                                             320 344 C2H2-TYPE.
350 374 C2H2-TYPE.
380 402 C2H2-TYPE.
415 AA; 44252 MW; 127A7B80DB3E33CC CRC64;
modified and this statement is not removed.
                entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Kidney;
MEDLINE-20440192; PubMed-10982849;
                                                          EMBL; AF317225; AAG38597.1; -. EMBL; AKO09739; BAB26470.1; -. EMBL; BCO13486; AAH13486.1; -. HSSP; PO8047; 1SP2.
                                                                                                                      MGD; MGI:1929988; K1f15.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00009; Zf-C2H2; 3.
ProDom; PD000003; Znf_C2H2; 1.
SWART; SM00355; ZnF_C2H2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB029254; BAA88561.1; -. HSSP; P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                              91.7%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the CLCNKA promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zinc finger repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ymphoid tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                       391 RSDHLSK 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Human)
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          1 RSDHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                             ;
9
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Q9UIH9;
                                                                                                                                                                                                                                                                                                              SEQUENCE
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RC STRAINBERKELS,

RX MEDLINE-20196006; bubbed=10731132;

RRADAMS M.D. Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Hilp.W., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Hilp.W., Hoskins R.A., Galle R.F.,

RA Adams M.D., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Balazej R.G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

Besson K.Y., Benos P.V., Berman B.P., Brottier P.,

Rockova D., Botchan M.R., Buuck J., Brokstein P., Brottier P.,

R. Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

R. Benos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

R. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Punkov B.C., Dunn P.,

R. Dodson K., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,

R. Hostin D., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

R. Harris N.L., Harvey D., Helman T.J., Wei M. H., Ibegwam C.,

R. Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Canton-S; TISSUE-Embryo;
MEDILNE-94081952; Pubbed-8259212;
Wimmer B.A., Jaeckle H., Pfeifie C., Cohen S.M.;
"A Drosophila homologue of human Spl is a head-specific segmentation
                                                                                                                         PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; DNA-binding; Activator; Nuclear protein;
Transcription regulation; DNA-binding; Activator; Nuclear protein;
DOMAIN 321 473 C2H2_TYPE.
ZN_FING 351 375 C2H2_TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                        Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                          6335F85141BEB276 CRC64;
                                                                                                                                                                                                                                                                                                                                                    91.7%; Score 33; DB 1; 85.7%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription factor BTD (Buttonhead protein).
BTD OR CG12653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     024266; Q9W319;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644 AA
                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                       Pfam; PF00096; zf-C2H2; 3.
ProDom; PD000003; Znf_C2H2; 1.
SMART; SM00355; ZnF_C2H2; 3.
                                         nterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                             43992 MW;
HGNC:14536; KLF15.
                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 366:690-694(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 RSDHLSK 398
                                                                                                                                                                                                                                        321
351
381
416 AA;
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                   ZN_FING
SEQUENCE
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Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
A Merkulov G., Milshina N.V., Mobarty C., Morris J., Moshrefi A.,
Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reses M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Welisschoach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A J.Y. Pek R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I.,
A J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng K. J., Welssen S. Shirk H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
INTERCALARY AND MANDIBULAR SEGNENTS OF THE HEAD.
INTERCALARY AND MANDIBULAR SEGNENTS OF THE HEAD.
                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Nuclear (By similarity).
DEVELOPMENTAL STAGE: FIRST EXPRESSED IN A STRIPE COVERING THE HEAD ANLAGEN OF THE SYNCITIAL BLASTODERM EMBRYO, PERSISTS THROUGH GASTRULATION AND DECAYS DURING GERM BAND EXTENSION. EXPRESSED LATER IN DEVELOPMENT IN A COMPLEX SPATIALLY RESTRICTED PATTERN.
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ProDom; PD000003; Znf_C2H2; 1.
SMART; SM00365; Znf_C2H2; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; Activator; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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A0DB98C2AF938452 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; Repeat.
ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2H2-TYPE.
C2H2-TYPE.
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POLY-ALA.
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POLY-PRO.
POLY-THR.
POLY-SER.
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EMBL; AE003448; AAF46518.1; -.
HSSP; P08047; 1SP2.
FlyBase; FBgn0000233; btd.
Interpro; IPR000822; 2nf_C2H2.
Pfam; PF00096; zf-C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68581 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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ZN_FING
ZN_FING
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784 AA

PRT;

STANDARD;

SP4_HUMAN Q02446; O60402;

S B

RESULT 4 SP4_HUMAN

111111: 402 RSDHLSK 408

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1 RSDHLSR 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OZETSKY P., Holmes A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS TO GT AND GC BOXES PROMOTERS ELEMENTS. PROBABLE
TRANSCRIPTIONAL ACTIVATOR.
                                                                                                                                                                                                                                                                                                  TISSUE-Uterus;
MEDLINE-93087156; PubMed=1454515;
Hagen G., Mueller S., Beato M., Suske G.;
"Cloning by recognition site screening of two novel GT box binding profelns: a family of Spl related genes.";
Nucleic Acids Res. 20:5519-5525(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- TISSUE SPECIFICITY: ABUNDANT IN BRAIN.
                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation; Activator; Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat.
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Pred. No. 11;
1; Mismatches 0; Indels
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-> A (IN REF. 2).
3C4EAE28CB2B81FB CRC64;
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HA -> QP (IN REF. 2).
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
TISTANSTIPLION factor Sp4 (SPR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC FINGERS.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 3.
PRINTS; PR00048; ZINCFINGER.
ProDom; PD000003; Znf_C2H2; 2.
SNART; SM00355; ZnF_C2H2; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_1; 3.
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POLY-ALA.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Nuclear.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X68561; CAA48563.1; -. EMBL; AC004595; AAD12226.1; PIN; S26638, S26638. HSSP: PO8947; 1SP1. TRANSFAC; T02339; -.
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ilarity 85.7%;
Conservative
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RSDHLSK 724
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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CONFLICT
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  SOLUTION OF STREET STRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kadonaga J.T., Carner K.R., Masiarz F.R., Tjian R.; "Isolation of cDNA encoding transcription factor Spl and functional analysis of the DNA binding domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89003041; PubMed-3139301;
Jackson S.P., Tjian R.;
"O-glycosylation of eukaryotic transcription factors: implications for mechanisms of transcriptional regulation.";
                                                                                                                                                                                                                                                                                                                                                                      Takahara T., Kanazu S., Yanagisawa S., Akanuma H.;
Herterogeneous Spl mRNAs in human HepG2 cells include a product of
homotypic trans-splicing";
J. Biol. Chem. 275:38067-38072(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION OF SEROTONIN 1A RECEPTOR PROMOTER BINDING SITES.
MEDLINE-96224025; Pubmed-8626793;
Parks C.L., Shenk T.;
"The serotonin lareceptor gene contains a TATA-less promoter that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: O-GLYCOSYLATED; CONTAINS N-ACETYLGLUCOSAMINE SIDE CHAINS. SIMILARITY: BELONGS TO THE SP1 FAMILY OF C242-TYPE ZINC-FINGER
                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla; Eutheria; Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 90-785 FROM N.A., AND SEQUENCE OF 359-375 AND 670-675 MEDLINE-88080466; PubMed-3319186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97218212; PubMed-9065444;
Narayan V.A., Kriwacki R.W., Caradonna J.P.;
Structures of Zinc finger domains from transcription factor Spl.
Insights into sequence-specific protein-DNA recognition.";
J. Biol. Chem. 272:7801-7809(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    responds to MAZ and Spl.";
J. Biol. Chem. 271:4417-4430(1996).
-!- FUNCTION: BINDS TO GC BOX PROMOTERS ELEMENTS AND SELECTIVELY
ACTIVATES MRNA SYNTHESIS FROM GENES THAT CONTAIN FUNCTIONAL
RECOGNITION SITES. CAN INTERACT WITH G/C-RICH MOTIFS FROM
SEROTONIN RECEPTOR PROMOTER.
                                                                                                                                                                                                                                                  SEQUENCE OF 4-785 FROM N.A.
TISSUE-GERVICAL CARCINOMB;
Haggart M.H., Ladurner A.G.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                          SPI_HUMAN STANDARD; PRT; 785 AA. P08047; Q9MYE7; Q9H3Q5; 01-A0G-1988 (Rel. 08, Created) 1-6CGT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 654-684 AND 684-712.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-558 FROM N.A.
MEDLINE-20545561; Pubmed-10973950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear.
                                                                                                                               Transcription factor Spl. SP1 OR TSFP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 51:1079-1090(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 55:125-133(1988).
                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O-GLYCOSYLATION
            RESULT 5
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EMBL; AF252284; AAF67726.1; -. EMBL; AB039286; BAB13476.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Imataka H., Sogawa K., Yasumoto K., Kikuchi Y., Sasano K., Kobayashi A., Hayami M., Fujii-Kuriyama Y.; "Two regulatory proteins that bind to the basic transcription element (BTE), a GC box sequence in the promoter region of the rat P-450IA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
                                                                                                                                                                                                                SMART; SMOUDES); ALL CALL, 13.
PROSTTE; PSO01029; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; Activator; Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat; Glycoprotein; 3D-structure. DOMA.N
ZINC_FINGERS.
ZINC_FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Nuclear.
-!- PTM: O-GLYCOSYLATED; CONTAINS N-ACETYLGLUCOSAMINE SIDE CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene.";
EMBO J. 11:3663-3671(1992).
-i- FUNCTION: BINDS TO GC BOX PROMOTERS ELEMENTS AND SELECTIVELY
ACTIVATES MRNA SYNTHESIS FROM GENES THAT CONTAIN FUNCTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                    C2H2-TYPE.
C2H2-TYPE.
D -> G IN REF. 3; AA SEQUENCE)
S -> F (IN REF. 3; AA SEQUENCE)
43893DBF651889EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created).
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            788 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93010958; PubMed-1356762;
                                                                                                                                              InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 3.
ProDom; PD000003; Znf_C2H2; 2.
SMART; SM00355; ZnF_C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                80693 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                91.7%;
85.7%;
EMBL; J03133; AAA61154.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Franscription factor Spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                         GlycoSuiteDB; P08047; - Genew; HGNC:11205; SP1.
               PDIR; A29635; A29635.
PDB; 1SP1; 21-APR-97.
PDB; 1SP2; 21-APR-97.
TRANSFAC; T00759; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111111:
697 RSDHLSK 703
                                                                                                                                                                                                                                                                                                                                                                                           670
785 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RSDHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEINS.
                                                                                                                              MIM; 189906
                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SP1_RAT
Q01714;
                                                                                                                                                                                                                                                                                                                                        ZN_FING
                                                                                                                                                                                                                                                                                                                                                            ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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us-10-006-069a-68.rsp

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InterPro; IPR000822; znf_C2H2.
Pfam; PF00096; zf-C2H2; 3.
SMART; SM00355; znF_C2H2; 3.
                                                                                                                                                                                                                                    86.1%;
            AL050309; CAB65785.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X74599; CAA52677.1;
AAC99849.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 86.1
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
           ENBL; AL050309; CAB6578
HSSP; P08047; 1SP2.
Genew; HGNC:6351; KLF8.
MIM; 300286; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 41,
                                                                                                                                                                                  334 3
263 2
359 AA;
                                                                                                                                                                                                                                                                                                         345 RSDHLS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 AA;
                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                   1 RSDHLS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RSDHLS 6
                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                      LCYB_SYNP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
SEQUENCE
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                 CONFLICT
                                                                                                                                                            ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                   055276;
                                                                                                                                                                        ZN_FING
                                                                                                                                                                                   ZN_FING
                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                              RESULT 8
LCYB_SYNP7
                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gorski J.L., MacDonald M., Vananthwerp M., Burright E.N., Bialecki M.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wray P.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Transcriptional repressor. Binds to CACCC-boxes promoter
                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Krueppel-like factor 8 (Zinc finger protein 741) (Basic kruppel-like
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SÜBÜNIT: Associates with CtBP.
-1- SÜBÜNIT: Accarion: Nuclear.
-1- TISSÜE SPECIFICITY: Ubiquitous.
-1- SIMILARITY: BELONGS TO THE SPI FAMILY OF C2H2-TYPE ZINC-FINGER
                                                                                                      PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; Activator; Zinc-finger; Metal-binding;
DNA-binding; Nuclear protein; Repeat; Glycoprotein.

ZINC_FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=20221593; PubMed=10756197;
van Vliet J., Turner J., Crossley M.;
Human Kruppel-like factor 8: a CACCC-box binding protein that associates with Ctab and represses transcription.";
Nucleic Acids Res. 28:1955-1962(2000).
                                                                                                                                                                                                                                 Score 33; DB 1; Length 788;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                        81015 MW; AA2B0CAB81AAB80C CRC64;
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                     359 AA.
                                                                                                                                                                                                                                             Pred. No. 11;
1; Mismatches
                                                                                                                                                                                  C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                        C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                   PRINTS: PR00048; ZINNEINGER.
Probom; PD000003; Znf_C2H2; 2.
SMART; SM00355; ZnF_C2H2; 3.
                     HSSP; P08047; ISPI.
TRANSFAC; T00754; -
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 3.
                                                                                                                                                                                                                               Query Match 91.7%;
Best Local Similarity 85,7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-299 FROM N.A.
D12768; BAA02235.1;
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLF8 OR ZNF741 OR BKLF3.
                                                                                                                                                                                                                                                                                             111111:
700 RSDHLSK 706
              JS0747; JS0747.
                                                                                                                                                                                            689 7
788 AA;
                                                                                                                                                                                                                                                                                1 RSDHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                095600; Q9UGC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                   KLF8_HUMAN
                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                          DOMAIN
ZN_FING
                                                                                                                                                                                  ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                         KLF8_HUMAN
                                                                                                                                                                                                                                                                                                                                            RESULT 7
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                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                       Gaps
PROSITE; PSO0028, ZINC_FINGER_C2H2_1; 3.
PROSITE; PSO0157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; Repressor; Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2). Bacteria; Cyanobacteria; Chroococcales; Synechococcus. NCBL_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.1%; Score 31; DB 1; Length 411; 100.0%; Pred. No. 15; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         Score 31; DB 1; Length 359;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: Carotenoid biosynthesis.
-!- SIMILARITY: BELONGS TO THE LYCOPENE CYCLASE FAMILY.
                                                                                                                                                                                                    E -> G (IN REF. 1).
F8FDCC1FD477C04F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAD (POTENTIAL).
C46CC5B2E85E7AC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHYLPHENOXY) TRIETHYLAMINE HYDROCHLORIDE (MPTA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000205; NAD_binding.
Oxidoreductase; NAD; Carotenoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 AA.
                                                                                                                                                                                                                                                                                       100.0%; Prec. ...
                                                                                                       ZINC FINGERS.
                                                                                                                                                   C2H2-TYPE.
C2H2-TYPE.
                                                                                                                               C2H2-TYPE.
                                                                              Nuclear protein; Repeat.
274 356 ZINC FIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopene beta cyclase (EC 1.14.-.-).
CRIL OR LCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
                                                                                                                                                                                                                          39313 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46085 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94120483; Pubmed-8291025;
Ohe N., Yamasaki Y., Sogawa K., Inazawa J., Ariyama T., Oshimura M.,
Fujii-Kuriyama Y.;
                                                                                                                                                                                                                                      [2]
SEQUENCE OF 1-31 FROM N.A.
MEDLINE-94327649; PubMed-8051167;
Imataka H., Nakayama K., Yasumoto K., Mizuno A., Fujii-Kuriyama Y.,
                                                                                                                                                                                            'Chromosomal localization and cDNA sequence of human BTEB, a GC box
                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 269:20668-20673(1994).

-!- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO GC BOX PROMOTER ELEMENTS. SELECTIVELY ACTIVATES MRNA SYNTHESIS FROM GENES CONTAINING TANDEM REPEATS OF GC BOXES BUT REPRESSES GENES WITH A SINGLE GC BOX.
                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                   Hayami M.;
"Cell-specific translational control of transcription factor BTEB
expression. The role of an upstream AUG in the 5'-untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; DNA-binding; Nuclear protein; Repeat; 21nc-finger; Metal-binding.
    protein 1) (GC box binding protein 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2D1B5A5BB9D42221 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASP/GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 13;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZINC FINGERS
                                                                                                                                                                                                       binding protein.";
Somat. Cell Mol. Genet. 19:499-503(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.3%; Score 30; 71.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 3.
PRINTS; PR00048; ZINCFINGER.
PRODOM; PD000003; Znf_C2H2; 1.
SWART; SW00355; ZnF_C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27234 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D31716; BAA06524.1; -.
EMBL; S72504; AAD14110.1; -.
HSSP; P08047; ISP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:1123; BTEB1.
    protein 1) (BTE-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                 (Krueppel-like factor
BTEB1 OR BTEB OR KLF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11111::
214 RSDHLTK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 AA;
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSDHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFAC; T02212;
                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 602902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BTE1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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    e S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-20541714; PubMed-11087666;
Scohy S., Gabant P., Van Reeth T., Hertveldt V., Dreze P.-L.,
Van Vooren P., Klviere M., Szpirer J., Szpirer C.;
"Identification of KLF13 and KLF14 (SP6), novel members of the SP/XKLF
transcription factor family.";
Genomics 70:93-101(2000).
-I- SUBCELLUIAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       -1- TISSUE SPECIFICITY: Ubiquitous.
-1- SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
                                                                                                                                                                                                              Eukaryota; Metaroa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BTEL_HUMAN STANDARD, PRT; 244 AA.

Q13866; Q16196;

15-DEC-1998 (Rel. 37, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Transcription factor BTEB1 (Basic transcription element binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO0028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; DNA-binding; Nuclear protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
SP6 OR KLF14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.3%; Score 30; DB 1; Length 152; 71.4%; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF629C4845599938 CRC64;
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                                                                                           152 AA
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC FINGERS.
C2H2-TYPE.
C2H2-TYPE.
                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1992575; Sp6.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00006; zf-C2H2; 3.
ProDom; PD000003; Znf_C2H2; 1.
SWART; SM00355; ZnF_C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ275988; CAC06698.1; -. HSSP; P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16456 MW;
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NON_TER 1 1
DOMAIN 30 112
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                                                                                             STANDARD;
                                                                                                                                                                                                    Mus musculus (Mouse)
181 RSDHLS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 RSDHLAK 107
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5; Conser
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                                                                                           SP6_MOUSE
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Best Local
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                                                                            SP6_MOUSE
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ö Gaps ö BTEL_MOUSE 035739;

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P58334;
15-JUN-2002 (
15-JUN-2002 (
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ZN_FING
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BTE4 MOUSE
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    δλ
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                                                                                                                                                                                                                    "Transcriptional regulation of the AP-2alpha promoter by BTEB-1 and AP-2rep, a novel wt-1/egr-related zinc finger repressor.";
Mol. Cell. Biol. 19:194-204(1999).

-i- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO GC BOX PROMOTER ELEMENTS. SELECTIVELY ACTIVATES MRNA SYNTHESIS FROM GENES CONTAINING TANDEM REPEATS OF GC BOXES BUT REPRESSES GENES WITH A SINGLE GC BOX.

-i- SUBCELLULAR LOCATION: Nuclear.
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-UNN-2002 (Rel. 41, Last annotation update)
Transcription factor BTEB1 (Basic transcription element binding protein 1) (BTE-binding protein 1) (GC box binding protein 1)
(Krueppel-1ike factor 9).
BTEB1 OR BTEB-1 OR BTEB OR KLF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR00082; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 3.
PRINTS; PR00048; ZINCFINGER.
PRODOM; PR000003; Znf_C2H2; 1.
SMART; SM00355; ZnF_C2H2; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; DNA-binding; Nuclear protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription factor BTEB1 (Basic transcription element binding
protein 1) (BTE-binding protein 1) (GC box binding protein 1).
BTEB1 OR BTEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                              Schuierer M., Werner O., Moser M., Roth C., Bauer R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 1; Length 244; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C2H2-TYPE.
C2H2-TYPE.
BBDF607FFA218D5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC FINGERS,
C2H2-TYPE,
                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BALB/c; TISSUE-Brain;
MEDLINE-99077958; PubMed-9858544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27169 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 83.3%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y14296; CAA74671.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFAC; T04700; -. MGD; MGD; MGI:1333856; KIF9.
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                                                                                           (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
143
173
173
203
244 AA;
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                                                                                                                               NCBI_TaxID=10090;
                                                                                           musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc-finger;
                                                                                                                                                                                              Imhof A., Sc
Buettner R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          P08047
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ZN_FING
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BTE1_RAT
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription factor BTEB4 (Basic transcription element binding-
protein 4) (BTE-binding protein 4) (Krueppel-like factor 16) (Dopamine receptor regulating factor).
KLF16 OR BTEB4 OR DRRF.
                                                                                                                                                                                 MEDLINE=93010958; PubMed=1356762;
Imataka H., Sogawa K., Yasumoto K., Kikuchi Y., Sasano K.,
Kobayashi A., Hayami M., Fujii-Kuriyama Y.;
Kobayashi A., Hayami M., Fujii-Kuriyama Y.;
Two regulatory proteins that bind to the basic transcription element (BTE), a GC box sequence in the promoter region of the rat P-4501Al gene.;
EMBO J. 1.3663-3671(1992).
I. 1.3663-3671(1992).
I. FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO GC BOX PROMOTER ELEMENTS. SELECTIVELY ACTIVATES MRNA SYNTHESIS FROM GENES CONTAINING TANDEM REPEATS OF GC BOXES BUT REPRESSES GENES WITH A SINGLE GC BOX.

A SINGLE GC BOX.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIRS. JS0748. JS0748.

HSSP, P08047: 1SP2.

HRANSFAC: T02210.

InterPro: IPR00822: Znf_C2H2.

PRINTS: PR00048: ZnCZH2; 3.

PRINTS: PR00048: ZnCZH2; 3.

PRODM: PR000003: Znf_C2H2; 3.

PROSTTE: PS00028: ZINC_FINGER.

PROSTTE: PS00127: ZINC_FINGER.C2H2_1; 3.

PROSTTE: PS01157: ZINC_FINGER.C2H2_2; 3.

Transcription regulation; DNA-binding; Nuclear protein; Repeat; Zinc_finger; Metal-binding.
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0
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FBD1D13FEAFA37E0 CRC64;
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C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C2H2-TYPE.
C2H2-TYPE.
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143
173
203
244 AA;
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                                                                                                                                      SEQUENCE FROM N.A.
                                                                                   NCBI_TaxID=10116;
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sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLFD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                            ZN_FING
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        NFING
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                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2012 (Rel. 41, Last annotation element binding-protein 4) (BTE-binding protein 4) (Krueppel-like factor 16) (Novel Spl-11ke zinc finger transcription factor
                                                                                                                                                                                                 and repression subdomains and also can mediate protein-protein
                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER
                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; DNA-binding; Nuclear protein; Repeat; Zinc-finger; Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
         TISSUE-Neuroblastoma;
MEDLINE-21309923; PubMed-11390978;
HWADLINE-21309923; PubMed-11390978;
HWADL C.K., D'Souza U.M., Elsch A.J., Yajima S., Lammers C.-H
Wang Y., Lee S.-H., Kim Y.-M., Nestler E.J., Mouradian M.M.;
"Dopanine receptor requiating factor, DRRF: a zinc finger transcription factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 1; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3F0D7739B1A09FA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                            ALA/PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO/SER-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                          EMBL; AF283891; AAK66968.1; -.
MGD; MGI:2153049; Klf16.
TRANSFAC; T05053; -.
                                                                                                                                                                                                                                                                                                                                                  TRANSFAC; T05053; -.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 3.
SMART; SM00355; ZnF_C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25665 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 71.4 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR BTEB4 OR NSLP2.
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RSDHLTK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                     103
126
126
126
156
186
223
223 23
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                                                                                                                                                                                                          Interactions
                                                                                                                                                                                                                              PROTEINS
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Q9BXK1;
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KLF16
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                    Conley A., Urrutia R.;

"Isolation of a novel zinc finger transcription factor from the pancreas extends the repertoire of Spi-like proteins present in this organ (Abstract #153).";

Pancreas 21:437-437(2000).

-I- FUNCTION: Transcription factor that binds GC and GT boxes and displaces Spi and Sp3 from these sequences. Modulates dopaminergic transmission in the brain (By similarity).

-I- SUBCELDILAR LOCATION: Nuclear (By similarity).

-I- SUBCELDILAR LOCATION: Unclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   097279; 097356;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation factor 13 (Faranscription element binding protein 3) (BTE-binding protein 3)
(RANNESS factor of late activated T lymphocytes-1) (RFLAT-1)
(Transcription factor NSLP1) (Novel Spl-11ke zinc finger transcription factor 1) (Transcription factor NSLP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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9A0CB4B1A585A118 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC FINGERS.
C2H2-TYPE.
C2H2-TYPE.
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SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30;
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71.4%;
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Best Local Similarity 71.4",
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC:16857; KLF16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 RSDHLAK 204
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157
187
210
252 AA;
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                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEINS.
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MIM; 606139;
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Search completed: July 15, 2003, 12:53:29
Job time: 7.66667 secs
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                               MEDLINE-99146379; PubMed-10023774;
Song A., Chen Y.F., Thamatrakoln K., Storm T.A., Krensky A.M.;
"RFLAT-1: a new zinc finger transcription factor that activates RANTES
gene expression in T lymphocytes.";
Immunity 10:93-103(1999).
                                                                                                                                                                                                                                                                                                                                                                                                         Kaczynski J., Zhang J.S., Ellenrieder V., Conley A., Duenes T.,
Kester H., van Der Burg B., Urrutia R.;
"The Sp11ike Protein BrEB3 inhibits transcription via the basic
transcription element box by interacting with mSin3A and HDAC-1
co-repressors and competing with Spl.";
J. Biol. Chem. 276:36749-36756(2001).
-! FUNCTION: Represses transcription by binding to the BTE site, a
GC-rich DNA element, in competition with the activator SPl. It
also represses transcription by interacting with the co-repressor
Sin3A and HDAC1. Activates RANTES expression in T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription requlation; Activator; Repressor; DNA-binding;
Nuclear protein; Repeat; Zinc-finger; Metal-binding; Phosphorylation.
DOMAIN
2 145
ALA/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLUIAR LOCATION: Nuclear.
TISSUE SPECIFICITY: Ubfquitous.
DOMAIN: The Ala/Pro-rich domain may contain discrete activation and repression subdomains and also can mediate protein-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: Phosphorylated.
-!- SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER
                                                                                                                                                                                           Cook T., Gebelein B., Urrutia R.; "Spl and its likes: biochemical and functional predictions for a "Spl and its likes: biochemical and functional predictions for a growing family of zinc finger transcription factors."; Ann. N.Y. Acad. Sci. 880:94-102(1999).
                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARG/INS-RICH (BASIC).
ZINC FINGERS.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                             TISSUE=Pancreas;
MEDLINE=99344343; PubMed=10415854;
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21453359; PubMed=11477107;
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EMBL, AF15628; AAD34020.1; --
EMBL, BC013946.1; --
EMBL, BC010438; AAH10438.1; --
EMBL, BC012441; AAH1241.1; --
HSSP. P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000822; Znf_C2H2.
Pfam; PF00009; Zf_C2H2; 6.
ProDom; PD000003; Znf_C2H2; 1.
SMART; SM00355; ZnF_C2H2; 3.
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                                                                                                                                        SEQUENCE FROM N.A.
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T05051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interactions.
                                                                                                                                                                                                                                                                                                                         Strausberg R.;
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                                                                                                                                                                                                                                                                                                    TISSUE-Lung;
                                                                                                                                                                                                                                                                                                                                                                           FUNCTION
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ZN_FING
ZN_FING
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6
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                                  A -> S (IN REF. 2),
EPTSPGABGAA -> MSPPPPALKARR (IN REF.
DD2765EE00E9C049 CRC64;
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0
                                                                             core 30; DB 1; Length 288; red. No. 16; Mismatches 0; Indels
                                                                                  Score 30;
Pred. No. 3
SER-RICH.
POLY-ALA.
                        POLY-ALA
                                                           31180 MW;
                                                                                 Query Match 83.3%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                        238 RSDHLTK 244
                                                           288 AA;
                                                                                                                                 1 RSDHLSR 7
                                  39
                        DOMAIN
CONFLICT
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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 15, 2003, 12:50:51; Search time 12.3333 Seconds (without alignments) 54.563 Million cell updates/sec Run on:

US-10-006-069A-68 36 1 RSDHLSR 7

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database:

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	hypothetical prote	•	scription	transcription fact	HF-1 requlatory el	SPR-1 protein - hu	regulatory protein		hypothetical prote	໘	hypothetical prote		¤	basic transcriptio		hypothetical prote	CO .	zinc finger protei		GT box-binding pro	ď	hypothetical prote	c	hypothetical prote				protein F14F4.3 [i	hypothetical prote
		ID	T22644	S30493 .	S39356	A29635	A48143	S26638	JS0747	JC5144	T27830	T25800	T33634	T26781	159602	JS0748	S25288	B83043	A57531	S52306	C83206	A44489	B70188	C24785	B44489	E96615	T32092	T30335	T20904	H89715	T20903
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		Length	1400	101	644	969	780	784	788	1464	264	309	497	233	244	244	244	411	469	480	491	495	608	899	. 269	1195	1355	1388	1400	40	1427
ф	Query	Match	100.0		91.7	91.7	91.7	91.7	91.7	91.7	86.1	86.1	86.1	83.3	83.3	83.3	83.3			83.3	83.3	83.3	ω.	83.3	83.3	83.3				83.3	83.3
		Score	36	33	33	33	33	33	33	33	31	31	31	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30
	Result	No.	-	7	٣	4	Ŋ	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	. 20	21	22	23	24	25	56	27	28	53

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Gaps

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Length 101; 0; Indels

Score 33; DB 2; Pred. No. 2.5; 1; Mismatches

91.7%; 85.7%;

Query Match Best Local Similarity 85.77

||||||: |5 RSDHLSK 21

1 RSDHLSR 7

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hypothetical prote soxA protein [impo	homeotic protein M	homeotic protein G	homeotic protein M	homeobox protein M	growth arrest-spec	conserved hypothet	probable C2H2-type	alpha-1-inhibitor	probable multifunc	protein kinase-lik	probable acetyl-Co	hypothetical prote	beta-1 bungarotoxi	beta-2 bungarotoxi
T07578 T46963	541469	A55641	A56837	B49122	N48130	H87447	F96743	A41081	. 863229	247546	T32413	T24490	TIKEBY	TIKEB2
77	7	~	7	7	~	7	7	~	H	7	~	7	-	т
103	298	302	303	303	303	315	413	609	864	934	2054	2251	59	61
80.6	90.8	90.6	90.6	90.6	90.6	90.6	90.8	9.08	90.6	90.6	90.6	90.6	77.8	77.8
29 80.6 29 80.6														

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A;Gene: CESP:F54D1.5
A;Map position: 4
A;Introns: 21/2; 51/2; 205/2; 276/3; 364/2; 394/2; 466/3; 507/3; 536/3; 599/3; 672/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
S30493
Spi protein - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C; Date: 330493
R; Chestier, A; Charnay, P.
DNA Seq. 2, 325-327, 1992
A; Title: Difference in the genomic organizations of the related transcription factors A; Reference number: S30493; MUID: 92338398; PMID:1633330
A; Accession: S30493
A; Status: prediminary
A; Molecule type: DNA
A; Residues: 1-101 <CHE>
A; Residues: 1-101 <CHE>
A; Cross-references: EMBL:X60136; NID:954158; PIDN:CAA42721.1; PID:e38120; PID:9133426
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                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:277132; PIDN:CAB00861.1; GSPDB:GN00022; CESP:F54D1.5
A;Experimental source: clone F54D1
C;Genetics:
hypothetical protein F54D1.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22644
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100.0%; Score 36; DB 2; Length 1400;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                       R.Lennard, N. submitted to the EMBL Data Library, July 1996
A.Reference number: 219592
A.Accession: T22644
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: A.Molecule 11400 <ALL.>
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51 RSDHLSR 57
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Gaps

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C; Accession: A48143
R; Zhu, H.; Nguyen, V.T.; Brown, A.B.; Pourhosseini, A.; García, A.V.; van Bilsen, M.; Mol. Cell. Biol. 13, 4432-444, 1993
A; Title: A novel, tissue-restricted zinc finger protein (HF-1b) binds to the cardiac A; Reference number: A48143; WUID:93309478; PMID:8321243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulatory protein Spl - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 01-Dec-2000
C;Accession: JS0747; S25287
R;Imacaka, H; Sogawa, K.; Yasumoto, K.; Kikuchi, Y.; Sasano, K.; Kobayashi, A.; Haya
submitted to JIPID, September 1992
A;Reference number: JS0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-788 < IMA>
A; Residues: 1-788 < IMA>
A; Cross-references: DDBJ: D12768; NID: 9220911; PIDN: BAA02235.1; PID: d1002730; PID: 9220
A; Cross-references: DDBJ: D12768; NID: 9220911; V.; Sasano, K.; Kobayashi, A.; Haya EMBO J. 11, 3663-3671, 1992
A; Title: Two regulatory proteins that bind to the basic transcription element (BTE), A; Reference number: $25287; MUID: 93010958; PMID: 1356762
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S26638
R.Hagen, G.; Mueller, S.; Beato, M.; Suske, G.
Nucleic Acids Res. 20, 5519-5525, 1992
A;Title: Cloning by recognition site screening of two novel GT box binding proteins: A;Reference number: S26638; MUID:93087156; PMID:1454515
A;Accession: S26638
                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SER-1 protein - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Residues: 1-780 < ZHU>
A;Experimental source: neonatal heart
A;Experimental source: neonatal heart
A;Note: sequence extracted from NCBI backbone (NCBIN:134660, NCBIP:134661)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: 1-784 <HAG>
A;Cross-treferences: EMBL:X68561; NID:g38419; PIDN:CAA48563.1; PID:g38420
C;Genetics:
A;Gene: GDB:SP4; SPR-1
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Pred. No. 25;
1; Mismatches
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Pred. No. 25;
1; Mismatches
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A;Map position: 2q31-2q31
C;Keywords: DNA binding; transcription regulation
       - rat
HF-1 regulatory element binding protein
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Best Local Similarity 85.7%;
Matches 6; Conservative
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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C; Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 05-Nov-1999
C; Accession: A29635; G4425
R; Kadonaga, J.T.; Carner, K.R.; Masiarz, F.R.; Tjian, R.
Cell 51, 1079-1090, 1987
A; Title: Isolation of cDNA encoding transcription factor Spl and functional analysis of A; Reference number: A29635; MUID:88080466; PMID:3319186
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A;Reference number: A44256; MUID:93052398; PMID:1427894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:J03133; NID:9339517; PIDN:AAA61154.1; PID:9339518
R;Ragoussis, J.; Senger, G.; Mockridge, I.; Sanseau, P.; Ruddy, S.; Dudley, K.; Sheer,
Genomics 14, 673-679, 1992
                                                                                                                                                                 Cispecies: Drosophila sp.
Cispecies: 38356
Cispecies: 3
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C;Keywords: DNA binding; transcription regulation; zinc finger
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A; Note: sequence extracted from NCBI backbone (NCBIP:125980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: Z29361; NID: 9441283; PID: 9441284
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                                                                                                                                          transcription factor btd · fruit fly (Drosophila sp.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB
Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription factor Sp1 - human (fragment) N;Alternate names: finger protein ZNF76
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A;Introns: 245/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%;
85.7%;
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Best Local Similarity 85.7.
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A; Residues: 569-598 <RAG>
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608 RSDHLSK 614
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A; Residues: 1-696 <KAD>
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A;Gene: FlyBase:btd
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-497 <1AT>
A;Cross-references: EMBL:AF099922; PIDN:AAC71780.1; GSPDB:GN00021; CESP:F56F11.3
A;Experimental source: strain Bristol N2; clone F56F11
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T25800
C;Accession: T25800
R;Fulton, L.
Submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid F54H5.
A;Reference number: Z20089
A;Accession: T25800
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-309 <FUL>
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C.Sate: 29-0c1-1999 #sequence_revision 29-0ct-1999 #text_change 29-0ct-1999
C.Sate: 29-0c1-1999
R.Latreille, P.; Kramer, J.; Keppler, D.
submitted to the EmBL Data Library, October 1998
A.Secription: The sequence of C. elegans cosmid F56F11.
A.Reference number: 221379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein Y40BlA.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26781
                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U80952; PIDN:AAB38094.1; GSPDB:GN00020; CESP:mua-1
A;Experimental source: strain Bristol N2; clone F54H5
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86.1%; Score 31; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels
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A;Map position: 3
A;Introns: 46/1; 103/3; 168/1; 195/1; 294/1; 440/1; 470/1
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A; Accession: T26781
A; Status: prellminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-233 <WILL>
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submitted to the EMBL Data Library, December 1998
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A;Gene: CESP:mua-1
A;Map position: 2
A;Introns: 31/1; 178/2; 234/2; 273/2
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295 RSDHLS 300
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Rivasaki, H.; Suzuki, Y.; Sinohara, H.

J. Blochem. 120, 1167-1175, 1996

A; Title: Cloning and sequencing of cDNAs encoding plasma alpha-macroglobulin and murinog A; Reference number: JC5143; MUID:97164019; PMID:9010766

A; Contents: liver
A; Accession: JC5144
A; Accession: JC5144
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-1464 CIWA>
A; Cross-references: DDBJ:DB4339
C; Superfamily: alpha-2-macroglobulin
F;1-23/Domain: signal sequence #status predicted <SIG>
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Riwhite, S.
Riwhite, S.
Submitted to the EMBL Data Library, November 1996
A; Reference number: 220426
A; Accession: T27830
A; Accession: T27830
A; Residues: 1-264 < WIL>
A; Residues: 1-264 < WIL>
A; Residues: 1-264 < WIL>
A; Circossion: T283090; PIDN:CAB05008.1; GSPDB:GN00019; CESP:ZK337.2
A; Conetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Cavia porcellus (guinea pig)
C:Date: 31-Jan-1997 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999
C:Accession: JC5144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein ZK337.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27830
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C2H2-type zinc finger domain, WT1 homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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Pred. No. 51;
1; Mismatches 0; Indels
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100.0%; Pred. No. 21;
tive 0; Mismatches (
                                                                                                                    Score 33; DB 2;
Pred. No. 25;
1; Mismatches
       A; Residues: 1-122, 'L', 124-311, 'A', 313-788 <IM2> C; Keywords: DNA binding; transcription regulation
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85.7%;
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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A; Introns: 60/3; 107/2; 155/3
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| 1392 RSDHVSR 1398
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700 RSDHLSK 706
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Search completed: July 15, 2003, 12:55:30 Job time: 13,3333 secs
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214 RSDHLTK 220
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C;Dates: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C;Dates: 02-Jul-1996
R;Ohe, N.; Yamsaski, Y.; 55409
Somat. Cell Mol. Genet. 19, 499-503, 1993
Somat. Cell Mol. Genet. 19, 499-503, 1993
A;Title: Cirromosomal localization and cDNA sequence of human BTEB, a GC box binding prot A;Reference number: 159602; MUID:94120483; PMID:8291025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reference number: 155409; MUD:94327649; PMID:8051167
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A; Molecule type: mRNA
A; Residues: 1-244 <IMA>
A; Cross-references: DDBJ:D12769; NID: 9220677; PIDN: BAA02236.1; PID: d1002731; PID: 9220678
C; Keywords: DNA binding; transcription regulation
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R;Imataka, H.; Sogawa, K.; Yasumoto, K.; Kikuchi, Y.; Sasano, K.; Kobayashi, A.; Hayami,
submitted to JIPID, September 1992
A;Reference number: JS0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: GB:D31716; NID:9505081; PIDN:BAA06524.1; PID:91060891
JImataka, H.; Nakayaman, K.; Yasumoto, K.; Mizuno, A.; Fujii-Kuriyama, Y.; Hayami, M.
- Biol. Chem. 269, 20668-20673, 1994
JIIIe: Cell-specific translational control of transcription factor BTEB expression.
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C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Nov-1999
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Pred. No. 33;
2; Mismatches 0; Indels
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                                                   Length 233;
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                                                Score 30; DB 2; Pred. No. 31; 2; Mismatches
A; Introns: 13/1; 45/3; 99/2; 178/2
                                              Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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nes 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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206 RSDHLTK 212
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| RSDHLTK 220
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214 RSDHLTK 220
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R; Imataka, H.; Sogawa, K.; Yasumoto, K.; Kikuchi, Y.; Sasano, K.; Kobayashi, A.; Haya EMBO J. 11, 3663-3671, 1992
A;Title: Two regulatory proteins that bind to the basic transcription element (BTE), A;Reference number: $25287; MUID:93010958; PMID:1356762
A;Accession: $25288
A;Molecule type: mRNA
A;Residues: 1-244 <IMA>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
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Pred. No. 33;
2; Mismatches
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Best Local Similarity 71.4%;
Matches 5; Conservative
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- protein search, using sw model OM protein

; Search time 33.3333 Seconds July 15, 2003, 12:48:06 Run on:

(without alignments)
27.983 Million cell updates/sec

US-10-006-069A-55 35 1 DRSNLTR 7 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

.DAT:* .DAT:* .DAT:* /gcgdata/geneseq/geneseqp-embl/AA1989.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:* .DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:* /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1998.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:* /SIDS2/gcddata/geneseq/geneseqp embl/AA1982.DAT:*/SIDS2/gcddata/geneseq/geneseqp embl/AA1983.DAT:*/SIDS2/gcddata/geneseq/geneseq-embl/AA1984.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1984.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/AA1988.DAT:*/SIDS2/gcddata/geneseq/geneseqp-embl/A /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT; /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1992 /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1993 /SIDS2/gcgdata/geneseq/genesegp-embl/AA1995 A_Geneseq_101002:* 1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980. 2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Zinc protein recog	F2 zinc finger for	Human VEGF-targete							
qı	AAB84241	ABB83564	ABJ03793	ABJ03812	ABJ03813	ABJ03816	ABJ03824	ABJ03888	ABJ03910	ABJ03913
8	22	23	23	23	23	23	23	23	23	23
% Query Match Length DB ID	7	7	7	7	7	7	. 7	7	7	. ,
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	35	. 35	35	35	35	35	35	35	35	35
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# ALIGNMENTS

AAB84241 standard; peptide; 7 AA. AAB84241;

06-AUG-2001 (first entry)

Zinc protein recognition helix SBS9 for target DNA triplet GAC

Phenotype associated gene; zinc finger protein; cancer; nephritis; prostate hypertrophy; hematopoiesis; osteoporosis; obesity; cardiovascular disease; diabetes.

Synthetic.

WO200140798-A2

07-JUN-2001.

06-DEC-2000; 2000WO-US33086.

99US-0456100 06-DEC-1999; SANG-) SANGAMO BIOSCIENCES INC. Liu Q, Rebar EJ; Case CC,

WFI; 2001-374953/39.

Identifying genes associated with selected phenotype for research purposes, involves culturing cells transduced with nucleic acid encoding zinc finger proteins and assaying cells exhibiting selected 

us-10-006-069a-55.rag

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zinc finger protein sequence that is attracted to a ZFP
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Best Local Similarity luv...
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Jarvis E;
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                                                                                                                                         The specification describes a method for identifying genes associated with a selected phenotype. The method involves providing a library of nucleotide sequences encoding partially randomized zinc finger proteins, transducing cells with expression vectors, each comprising a sequence from the library, culturing the cells for expressing the zinc finger protein, assaying the cells for selected phenotype, and identifying the gene of interest, in cells exhibiting the phenotype. The method is useful for identifying a gene or genes associated with a selected phenotype such hematopolesis, osteoporosis, obesity, cardiovascular disease or diabetes. The method is useful in academic laboratories in the biotechnological industries, and in pharmaceutical, genomic, agricultural and chemical companies. AbB&433.44 represent recognition helices of zinc finger proteins, which recognise different DNA triplets.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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100.0%; Pred. No. 7.8e+05;
tive 0; Mismatches 0;
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                                                                              Example 1; Page 36; 58pp; English.
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11-MAY-2001; 2001US-290716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zinc finger protein; anglogenesis; vasculogenesis; ischaemia; diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary; antiuleer; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antilifertility.
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Pred. No. 7.8e+05;
100.0%; Score 35; DB 23; 100.0%; Pred. No. 7.8e+05;
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100.0%; Pr
tive 0;
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12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
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                                                                                                                  Homo sapiens.
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12-DEC-2000;
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                                                                                                                                                                                                                                                    diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antitatherosclerotic; vasotropic; antiarthritic; vulnerary; antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.
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Zinc finger protein; angiogenesis; vasculogenesis; ischaemia; diabetic retinopathy; psorlasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary; antiulcer; cytostatic; antipsorlatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth;
gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary;
antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VBGF) genes. The protein is useful for modulating expression of a VBGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of the gene and for treating atherosclerosis, ischemia, arthritis, wound or
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12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
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Best Local Similarity 100.
Matches 7; Conservative
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The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endochelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atheroscierosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of the gene and for treating atherosclerosis, ischemia, arthritis, wound or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zinc finger protein; anglogenesis; vasculogenesis; ischaemia; diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerai antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.
                    New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression cgene and for treating atherosclerosis, ischemia, arthritis, wound
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                                                                                                                       Claim 4; Page 102; 195pp; English
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Best Local Similarity 100..
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gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary;
antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological;
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                                                                                                                                                                                                                                                       New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of the gene and for treating atherosclerosis, ischemia, arthritis, wound or
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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                                                                                                                     SANG-) SANGAMO BIOSCIENCES INC
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                                      07-DEC-2000; 2000US-0733604.
12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
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06-DEC-2001; 2001WO-US46861.
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12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
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Jarvis E;
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diabetic retinopathy; pšoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary; antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological;
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                                                                                                                                                                                                                                                                                                                                               Human VEGF-targeted zinc finger protein fragment SEQ ID NO: 170.
                                                                                                                                                                                                                                                                                                                                                                                                           protein; angiogenesis; vasculogenesis; ischaemia;
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12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
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Matches 7; Conservative
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Jarvis E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linc finger protein; angiogenesis; vasculogenesis; ischaemia; diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasctropic; antiarthritic; vulnerary; antiuleer; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of the gene and for treating atherosclerosis, ischemia, arthritis, wound or
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treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psorlasis. The present sequence is a peptide shown in the invention.
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
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                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 7; Conservative
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Les 7; Conserv
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                                                                                                                             7 AA;
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Matches
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Eisenberg SP;

Wolffe A,

Liu P,

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Length 7;
                                  Indels
 100.0%; Score 35; DB 23; 100.0%; Pred. No. 7.8e+05;
                                  Mismatches
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06-DEC-2001; 2001WO-US46861.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary; antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.
                                                                                                                                                                                                                                                                            of the
                                                                                                                                                                                                                                                                                                                                      The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atherosociarosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention.
        Zinc finger protein; angiogenesis; vasculogenesis; ischaemia; diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiatheritic; vulnera antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                 New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression ogene and for treating atherosclerosis, ischemia, arthritis, wound
                                                                                                                                                                                                                 Jamieson A, Liu Q, Liu P, Wolffe A, Eisenberg SP;
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                                                                                                                                                                                                                                                                                                                     Disclosure; Page 105; 195pp; English.
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                                                osteopathic; antiinfertility
                                                                                                                               06-DEC-2001; 2001WO-US46861
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2000US-0736083
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nes 7; Conservative
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12-DEC-2000;
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                                                                   Rattus sp.
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ZFP: cytostatic; antidiabetic; ophthalmological; vasotropic; chromatin; gene expression; antirheumatic; antiarthritic; antipsoriatic; nootropic; neuroprotective; cerebroprotective; estrogen receptor alpha; ER-alpha;
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                                                                                                                                                                                                                                                                                                                                                      endothelial growth factor gene, useful for modulating expression of t
gene and for treating atherosclerosis, ischemia, arthritis, wound or
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                                                                                                                                                                             Eisenberg SP;
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                                                                                                                                                                                                                                                                                                                              target site in vascular
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                                                                                                                                                                             Liu Q, Liu P, Wolffe A,
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Pred. No. 7.8e+05;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                        New zinc finger protein that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 105; 195pp; English.
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07-DEC-2000; 2000US-0733604.
12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
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Best Local Similarity 100.0
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                                                                                                                                                                             Jamieson A,
                                                                                                                                                                                                                                                                 WPI; 2002-527918/56.
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The invention relates to regulating the expression of a gene residing in the chromatin of a cell. The method involves identifying one or more accessible regions in cellular chromatin associated with gene; designing a regulatory molecule comprises a DNA-conditional domain targeted to a sequence within the accessible region, and functional domain targeted to a sequence within the accessible region, and contacting the regulatory molecule with the cell.

The method is used for regulating the expression of a gene (e.g., a gene cancoding a nuclear receptor such as estrogen receptor alpha (ERRalpha), consolidating the expression of a gene (e.g., a gene catrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha (ERRalpha), constitutively active receptor alpha (ERRalpha), residing in the chromatin of a cell. Regulation of gene expression (such as nuclear receptor genes) will be useful in treatment of various cas nuclear receptor genes) will be useful in treatment of various cas nuclear receptor genes) will be useful in treatment of various carry out the regulation. The method is also useful for modulation of gene expression for therapeutic or prophylactic applications e.g., carry out the regulation. The method is also useful for modulation of disease, stroke, etc. The method also has applications in pharmaceutical arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's cunknown function. The method also facilitates development of tissue and cardinal models of disease states, duny validation, and therapeutic product development. The method also facilitates development of tissue and cardinal models of disease states, duny validation, and therapeutic product development. The method also allow identification of cardinal models of disease states, duny validation, and therapeutic product development. The method also allow identification of cardinal models of disease states, duny validation, and therapeutic product development.
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of cellular chromatin associated with a gene, and
                                                                                                    Example 1; Page 44; 64pp; English.
accessible region
                                    functional domain
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7 AA; Sednence

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Gaps
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           Length 7;
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
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ABB80812 standard; peptide; 7 AA. 23-SEP-2002 ABB80812; RESULT 14 ABB8081 

Human ER-alpha locus targeting ZFP3 peptide #4. (first entry)

cytostatic; antidiabetic; ophthalmological; vasotropic; chromatin; gene expression; antirheumatic; antlarthritic; antipsoriatic; nootropi neuroprotective; cerebroprotective; estrogen receptor alpha; ER-alpha; neuroprotective; cer zinc finger protein

Synthetic.

WO200244386-A2

30-NOV-2001; 2001WO-US45098. 06-JUN-2002.

01-DEC-2000; 2000US-250804P.

(SANG-) SANGAMO BIOSCIENCES INC

Collingwood T; Tse C, Wolffe AP,

WPI; 2002-537455/57

regulating expression of gene by contacting cell with regulatory molecule comprising DNA-binding domain targeted to sequence within accessible region of cellular chromatin associated with a gene, and functional domain

Example 1; Page 44; 64pp; English.

The invention relates to regulating the expression of a gene residing in the chromatin of a cell. The method involves identifying one or more accessible regions in cellular chromatin associated with gene; designing a regulatory molecule comprises a DNA-binding domain targeted to a sequence within the accessible region, and a functional domain; and contacting the regulatory molecule with the cell. The method is used for regulating the expression of a gene (e.g., a gene entrogen receptor beta (ERMetal, hepatocyte nuclear factor 4 alpha (FRRalpha), hepatocyte nuclear factor 4 alpha (FRRalpha), or constitutively active receptor alpha (ERMalpha)) residing in the chromatin of a cell. Regulation of gene expression (such as nuclear receptor genes) will be useful in treatment of various classases, including cancer, diabetes and cardiovascular disease, where the regulatory molecule as described above, is contacted with the cell to denote the regulation of the repulation of penespination of gene expression of carry out the regulation of the repulation of penespination of gene expression of such carry out the regulation of penespination of penespination of gene expression of carry out the regulation of penespination of gene expression of gene expression for the required view method is also useful for modulation of gene expression of gene expression for the required view of the regulation of the repulation of the repulation of the regulation unknown function. The method also facilitates development of tissue and animal models of disease states, drug validation, and therapeutic product development. The methods also allow identification of the role of nuclear receptors of unknown functions in cellular homeostasis. Sequences ABB6071-817 represent zinc finger protein (ZFP) DNA-binding domains that were fused to functional domains and tested for their ability to regulate expression of the ER in living cells. diabetic retinopathy, ischaemia, macular degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell anemia, Alzhaimer's disease, stroke, etc. The method also has applications in pharmaceutical research of both nuclear receptors of known function as well as those of

Seguence

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Gaps ö Length 7; Indels 100.0%; Score 35; DB 23; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Conservative Best Local Similarity Matches 7; Conserv Query Match

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1 DRSNLTR 7 1 DRSNLTR 7 ò g

RESULT 15

ABP48386 standard; Peptide; 7 AA. 

ABP48386;

28-AUG-2002 (first entry)

Zinc finger protein related peptide motif SEQ ID NO:395.

Zinc finger protein; ZFP; DNA binding protein; zinc finger.

Homo sapiens. Synthetic

WC200242459-A2.

30-MAY-2002.

20-NOV-2001; 2001WO-US43438.

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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) of a target site, comprising a first (FI), a second (F2), and a third (F3) of target site comprises, in 3'-5' direction, a first (SI), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (I) designing (I); (2) a polynucleotide (III) encoding (I) or (II); and (I) fings to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc that it binds to the S2 target subsite, thus designing (I) that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therefore and plant engineering. (I), (II) or (III) is useful in the subsite; therapeutic methods to modulate the expression of a target region within the subsite; and function of gene expression of a target region within a subject, in diagnostic methods for sequence specific detection of target uncleic acid in a sample, and in assays to determined the compoundation of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced the form of the factor of the subsite of the factor of the factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epresent DNA target sequences and zinc finger peptides which are given
                                                                                                                                                                                                                                                                        New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 37; 81pp; English
                                                                    (SANG-) SANGAMO BIOSCIENCES INC.
20-NOV-2000; 2000US-0716637.
                                                                                                                                                                                                          WPI; 2002-500284/53
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                                                                                                                                         Liu 0;
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100.0%; Score 35; DB 23; 100.0%; Pred. No. 7.8e+05; 11ve 0; Mismatches 0; Query Match
Best Local Similarity 100.
Matches 7; Conservative 1 DRSNLTR 7 DRSNLTR 7 á

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0; Gaps

Length 7; 0; Indels

Search completed: July 15, 2003, 12:53:00 Job time: 33.6667 secs

g

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 15, 2003, 12:50:51; Search time 12.3333 Seconds (without alignments) 54.563 Million cell updates/sec Run on:

US-10-006-069A-55 35 1 DRSNLTR 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_73:*

pirl:* pir2:* pir3:* .....

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	tagender 15 - empts		ப	ij		conserved hypothet	hypothetical 21.8K	hypothetical prote	-	. hypothetical prote	positive regulator	amidase-related pr	hypothetical prote	rfbD protein - Vib	GDP-D-mannose dehy	hypothetical prote	ס	GDP-mannose 4,6-de	GDP-d-mannose dehy	GDP-D-mannose dehy	GDP-D-mannose dehy	GDPmannose 4,6-deh	geranylgeranyl-dip	hypothetical prote		_	SPA2 protein - yea	ч	transcription fact
ΙD	E82491	H81997	S06584	A53044	T13953	AC0940	S40863	E91234	E86081	T45056	D86786	H87572	T36056	S70961	G90983	T44322	B85829	S28470	D64971	B90986	E8583.1	AB0769	B53044	D87637	T36919	T14748	9	69	A56922
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Query Match Length	530	125	140	377	1523.	198	199	199	199	220	276	304	305	362	372	372	372	373	373	373	373	373	377	381	533	540	1466	2529	2578
Query Match	91.4	85.7	2	85.7	85.7	82.9	82.9	ď.	'n.	ď	ď	ä	ς.	82.9	ä	82.9	ς.	'n	ä	ö	ς.	ς.		ς.	82.9	ς.		82.9	82.9
Score	32	30	30	30	30	29	29	59	53	53	29	29	29	29	29	29	29	29	29	29	29	. 29	29	29	29	29	53	29	29
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vasopressin / neur hypothetical prote	_ 5	hypothetical prote hypothetical repea	xylan 1,4-beta-xyl hybothetical prote	alpha-aminoadipyl-	arpha aminoacipyi 14K hypothetical t hypothetical profe		. — <u></u>
A29101 D71980	S57969	H84673 T41314	T00131	YGPLV3	E39741	S76649 H71700	'147832 AI0795
2 2	7	77 77	2 0	ı — -	100	100	77
144	319	347	798	3746	5/51 61 715	166	306
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28	78 78 78	58 58	28	7.83	27.	27	27
30	32 33	34 35	36	800	404	4 4 5 2 6	44 45

	 RESULT 1 E82491
	sigma-54 dependent transcription regulator VCA0182 [imported] - Vibrio cholerae (stra
	C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
	C, Accession: E82491 R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
_	Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
	Nature 406, 477-483, 2000
	 A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
	A; Reference number: A82035; MUID: 20406833; PMID:10952301
	A; Accession: E82491
	A; Status: preliminary
	A; Molecule type: DNA
	A; Residues: 1-530 <hei></hei>
	A; Cross-references: GB: AE004358; GB: AE003853; NID: 99657566; PIDN: AAF96095.1; GSPDB: GN
_	A; Experimental source: serogroup 01; strain N16961; biotype El Tor
	C; Genetics:
	A; Gene: VCA0182
	 A,Map position: 2
	Query Match 91.4%; Score 32; DB 2; Length 530;
_	Best Local Similarity 85.7%; Pred. No. 18; Matches 6: Conservative 1: Mismatches 0: Indels 0: Gaps 0:
	Qy 1 DRSNLTR 7 .

505 DRANLTR 511 g G

RESULT H81997

probable lipoprotein NMA0065 [imported] - Neisseria meningitidis (strain 22491 serogr C; Species: Neisseria meningitidis (c; Species: Neisseria meningitidis (c; Species: OS-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 (c; Accession: H81997 (c; Accession: H81997) (c; Accession: H81987) (c; Accession: H81997) (c; Accession: H81987) (c; Accession:

A; Status: preliminary A; Molecule type: DNA

A. Stesidues: 1-125 CPAR>
A. Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83381.1; PID:g737
A. Experimental source: serogroup A, strain Z2491

C;Genetics: A;Gene: NMA0065

C; Superfamily: Neisseria meningitidis probable lipoprotein NMA0065

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Ayouthetical 21.8K protein (tpia 3'region) precursor - Escherichia coli (strain K-12) Nylternate names: hypothetical protein f199
C;Species: Escherichia coli
C;Date: 19-May-1994 #sequence_revision 01-Sep-1995 #text_change 01-Mar-2002
C;Accession: $40863; C65198
R;Plunkett III, G;Burland, V; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 21, 3391-3398, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1938, 1937, 1453-1462, 1997
A;Tcoss-references: EMBL:19201; NID:3304961; PIDN:AAB03052.1; PID:3305023
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
                A;Title: Identification of high-molecular-weight proteins with multiple EGF-like moting A;Reference number: 214126; MUID:98360089; PMID:9693030
A;Accession: T13953
A;Accession: T1353
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1523 <NAK>
A;Residues: 1-1523 <NAK>
A;Cross-references: EMBL:AB011531; NID:g3449291; PIDN:BAA32461.1; PID:g3449292
A;Genetics:
A;Ge
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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church th, T.; Connerton, P.; Cronnerton, P.; Coronerton, P.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A; Accession: AC0940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein STY3788 [imported] - Salmonella enterica subsp. enteric
C; Species: Salmonella enterica subsp. enterica servoar Typhi
A; Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30; DB 2; Length 152
Pred. No. 1.6e+02;
2; Mismatches 0; Indels
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Best Local Similarity 71.4%;
Matches 5; Conservative 5
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A;Molecule type: DNA
A;Residues: 1-198 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  finger protein (clone XlcGF71.1) - African clawed frog (fragment)
C; Species: Xenopus laevis (African clawed frog)
C; Date: 28 Feb-1990 #sequence_revision 28 Feb-1990 #text_change 31-Dec-1993
C; Accession: S06584
R; Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Knoech A; Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Knoech A; Fitle: Second-order repeats in Xenopus laevis finger proteins.
A; Reference number: S05632; MUID: 90040698; PMID: 2509712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        geranylgeranyl-diphosphate geranylgeranyltransferase (EC 2.5.1.32) I beta chain - human C.Species: Homo sapiens (man)
C.Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Nov-1999
C.Accession: A53044
R.Zhang, F.L.; Diehl, R.E.; Kohl, N.E.; Gibbs, J.B.; Giros, B.; Casey, P.J.; Omer, C.A. J. Bloi. Chem. 269, 3175-3180, 1994
A;Title: CDNA cloning and expression of rat and human protein geranylgeranyltransferase A;Reference number: A53044; MUID:94140804; PMID:8106351
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NyAlternate names: slit protein homolog
NyAlternate names: slit protein homolog
Syecies: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2002
C;Accession: T13953
S;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
                                                                                                                Gaps
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                         Length 125;
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                             Score 30; DB 2; ; Pred. No. 12;
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85.7%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-140 <NIE>
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GDB:305477
C; Superfamily: cell division control protein CDC43
C; Keywords: transferase
85.7%; bcc.
100.0%; Pred. No. ...
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                    Query Match 85.7
Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conservative
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A;Molecule type: mRNA
A;Residues: 1-377 <ZHA>
                                                                                                                                                                                   1 DRSNLT 6
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Rivilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burto raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Jo B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. Nature 368, 32-38, 1994
A; Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E. tock, L.; Wilkinson-Sproat, J.; Wohldman, P.
A; Tille: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. A; Reference number: S43531; MUID: 94150718; PMID: 7906398
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A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Recus preliminary
A;Residues: 1-276 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  positive regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403) (S.Species: Lactococcus lactis subsp. lactis (S.Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 (S.Accession: D86786)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1.120 <WIL>
A; Cross-references: EMBL.AL132896; NID:g6434440; PIDN:CAB60935.1; PID:g6434470
A; Experimental source: clone Y39B6B
C; Genetics:
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A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                   C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Aug-2000
C;Accession: T45056
                                                                                                                                                                                                                                                                                                                          hypothetical protein Y39B6B.dd [imported] - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: Caenorhabditis elegans hypothetical protein Y39B6B.
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Pred. No. 36;
2; Mismatches
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A;Note: Y39B6B.dd
                 Mismatches
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71.4%;
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Best Local Similarity 71.4.
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Best Local Similarity 71.4.
مدت:
                 Conservative
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44 DKSNVTR 50
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                                                                                  1 DRSNLTR 7
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T45056
                 Matches
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A;Molecule type: DNA
A;Residues: 1-199 <STO>
A;Cross-references: GB:AE005174; NID:912518821; PIDN:AAG59113.1; GSPDB:GN00145; UWGP:254
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: E91234
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Basawara, N.; Yasaunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench A;Accession: E91234
A;Status: preliminary
                                                                A. Status: preliminary; nucleic acid sequence not shown; translation not shown A. Molecule type: DNA A. Molecule type: A. Molecule type: M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ECs4845 [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
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Pred. No. 32;
2; Mismatches 0; Indels
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A;Gene: ECs4845
C;Superfamily: Escherichia coli hypothetical protein yiiQ
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C;Superfamily: Escherichia coli hypothetical protein yiiQ
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C65198
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Pred. No. 32;
2; Mismatches (
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Pred. No. 32;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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71.4%;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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73 DKANLTR 79
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Length 220; Indels

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Length 276;
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                                                                                                     RESULT 12
H87572
amidase-related protein [imported] - Caulobacter crescentus
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Score 29; DB 2
Pred. No. 46;
2; Mismatches
DB .
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Gaps

Gaps

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Length 362; 1; Indels

DB 2; 61;

us-10-006-069a-55.rpr

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A,Molecule type: DNA
A;Residues: 1-372 <HAY>
A;Resizuez: references: GB:BA000007; PIDN:BAB36262.1; PID:g13362307; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                  Score 29; DB 2
Pred. No. 61;
0; Mismatches
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He: 13.3333 secs
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C;Superfam11y: GDP-D-mannose dehydratase
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Best Local Similarity 85...
6; Conservative
                                  Query Match 82.9
Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                   1 DRSNLTR 7
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C; Species: Caulobacter crescentus
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C; Accession: H8752
B; Accession: H8752
B; Laub, M.T.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, M. J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S. A. 98, 4136-4141, 2001
A; Fitle: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C. Accession: T36056
R. Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M. Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M. Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M. A. Reference number: 221595
A. A. Accession: T36056
A. Scatus: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: DNA
A. Residues: 1-305 <SAU>
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A,Gene: SCOEDB:SCD78.17c
C;Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH1C
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R; Bik, E.M.; Bunschoten, A.E.; Willems, R.J.L.; Chang, A.C.Y.; Mooi, F.R.
Mol. Microbiol. 20, 799-811, 1996
A; Title: Genetic organization and functional analysis of the otn DNA essential for cell-A; Reference number: S70952; MUID: 96386047; PMID: 873876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AL034355; PIDN:CAA22222.1; GSPDB:GN00070; SCOEDB:SCD78.17c A;Experimental source: strain A3(2)
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
C;Genetics:
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                                                                                                                                                                                                                                                                                                                  A;Gross-references: GB:AE005673; NID:913424186; PIDN:AAK24580.1; GSPDB:GN00148 C;Genetics:
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C;Species: Vibrio cholerae
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Streptomyces coelicolor
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
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Pred. No. 51;
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Pred. No. 51;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SCD78.17c - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                      82.9%; Scor.
100.0%; Pred. No. Jr.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: rfbD
C;Superfamily: GDP-D-mannose dehydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 82.9%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.9
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||:|:||
208 DRANVIR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111111
264 RSNLTR 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DRSNLTR 7
                                                                                                                                                                                                                                                           A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-304 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RSNLTR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S70961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
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Gaps

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Indels

;

Length 372;

DB 2;

# GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

July 15, 2003, 12:49:31; Search time 6.66667 Seconds (without alignments) 43.550 Million cell updates/sec

US-10-006-069A-55 35 1 DRSNLTR 7

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Description	008738 mus musculu	homo sap	xeno		guine	escheri		P32054 escherichia							strept										Q9wyd0 thermotoga		Q06828 homo sapien	P50608 mus musculu	σ		7	226 homo	Q05057 parsnip yel
SUMMAKIES		D	ICE6_MOUSE	ICE6_HUMAN	ZG71_XENLA	PGT1_HUMAN	VGLH_GPCMV	YIIQ_ECOLI	GMD2_VIBCH	GM4D_ECOLI	GMD1_VIBCH	PGT1_RAT	CYB_ARTCI	Z33A_HUMAN	SPA2_XEAST	NEU2_CAVPO	ARGC_STRCL	ACVS_PENCH	ACVT_PENCH	CCMD_BRAJA	RECA_SPIME	Y420_AQUAE	FMOD_RABIT	LUM_PIG	· Y516_SYNY3	UPPS_RICPR	PROB_THEMA	FMOD_BOVIN	FMOD_HUMAN	FMOD_MOUSE	FMOD_RAT		CBLB_HUMAN	- 1	POLG_PYFV1
		BB	1	-	-	Н	Н	-	Н	⊣	-	Н	-	-	-	Н	Н	Н	-	-	-	-	-	7	Ä	-	H	7	-	-	-	-	Η.	<b>-</b>	Н
		Length	276	293	140	377	722	199	372	373	373	377	379	810	1466	144	340	3746	3791	61	77	115	147	147	166	226	353	375	376	376	376	860	985	101	3027
ď	Query		98.6	88.6	85.7	85.7				82.9					٠					77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1	77.1
		Score	31	31	30	30	30	. 29	29	59	29	29	29	29	53	28	28	28	28	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27
	Result	No.	H	7	m	4	5	9	7	80	0	10	11	13	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	E

078429 guillardia P01185 homo sapien								
rk21_guith neu2_human	YP2C_STAAU 6PGL_SCHPO	VNST_UUK	YIAK_HAEIN	ETV2_MOUSE	HEMS_YEREN	HMUS_YERPE	TRPD_SYNY3	ICEB_MOUSE
нн		Н-	-	Н	Н	Н	-	٦
104 164	236	273	332	335	345	345	348	373
74.3	74.3	74:3	74.3	74.3	74.3	74.3	74.3	74.3
26 26	26 26	26	56 26	56	56	56	56	56
34 35	36 37	38	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1  TEGE MOUSE  TEGE MOUSE  TEGE MOUSE  TO 1-407-1997 (Rel. 35) Lesstence update)  TO 1-407-1997 (Rel. 34) Lesst annotation update)  TO 1-407-1997 (Rel. 34) Lesst annotation update)  TO 1-407-1997 (Rel. 34) Lesst annotation update)  TO 2-407-1907 (Rel. 41) Lesst annotation update)  TO 2-407-1907 (Rel. 41) Lesst annotation update)  TO 3-407-1907 (Rel. 41) Lesst annotation update)  TO 4-407-1907 (Rel. 41) Lesst annotation update)  TO 4-407-1909 (Rel. 41) Lesst annotation update)  TO 5-407-1909 (Rel. 41) Lesst annotation update)  TO 6-407-1909 (Rel. 41) Lesst annotation update)  TO 7-40-1909 (Rel. 41) Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41) Rel. 41 Lesst annotation update)  TO 8-408-1909 (Rel. 41)
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0; Mismatches
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C2H2-TYPE.
C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90040698; PubMed-2509712;
                                                                                                                                                                                                                                                                                                                                                                                                                        33409 MW;
                     EMBL; U20536; AAC50168.1; -. EMBL; U20537; AAC50169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.78;
                                                                 MEROPS; C14.005; -. Genew; HGNC:1507; CASP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; .Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                           193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                      1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DRSNLTR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 AA;
                                                                                                 MIM; 601532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZG71_XENLA
P18736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZN_FING
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
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ZN_FING
                                                                                                                                                                                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                                                                                             PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
ZG71_XENLA
                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBGUIT: HETERODIMEN OF A 18 KDB (P18) AND A 11 KDB (P11) SUBUNIT. SUBCELLULAR LOCATION: CYtoplasmic.
SUBCELLULAR LOCATION: CYtoplasmic.
ARE PRODUCTS: 2 ISOPORMS; ALPHA (SHOWN HERE) AND BETA;
ARE PRODUCED BY ALTERNATIVE STLCING. THE BETA ISOFORM DOES NOT SEEM TO HAVE PROTECLITIC ACTIVITY.
PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-F-cell;
MEDLINE-95316841; PubMed-7796396;
Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
"Mch2, a new member of the apoptotic Ced-3/Ice cysteine protease gene
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The Ced-3/interleukin lbeta converting enzyme-like homolog Mch6 and
the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mediator CPP32.";
J. Biol. Chem. 271:27099-27106(1996).

1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION: CLEAVES POLY(APP-RIBOSE)
POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOTES
PROGRAMMED CELL DEATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Lymphocytes;
MEDLINE-97059171; PubMed-8900201;
Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,
                                                                               CASPASE-6 SUBUNIT P18 (BY SIMILARITY).
BY SIMILARITY.
CASPASE-6 SUBUNIT P11 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G., Alnemri E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                  01-ocT-1996 (Rel. 34, Last sequence update)
15-70N-2002 (Rel. 41, Last annotation update)
Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
CASP6 OR MCH2.
                                                                                                                                                                                               Score 31; DB 1; Length 276;
                                                                                                                                                                                                                              1; Indels
                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
5965DE9321126B6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                 Hydrolase; Thiol protease; Apoptosis; Zymogen
PROPEP 1 5 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                         293 AA.
                                                                                                                                                                                                              Pred. No. 6.3
0; Mismatches
PS01121; CASPASE_HIS; 1.
PS50207; CASPASE_P10; 1.
PS50208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cancer Res. 55:2737-2742(1995)
                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                               31595 MW;
                                                                                                                                                                                           Similarity 85.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Human).
                                                                                                                                                                                                                                                                              || ||||||
53 DRDNLTR 59
                                                                                                                                                              276 AA;
                                                                                                                                                                                                                                                            DRSNLTR 7
                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                     ICE6_HUMAN
P55212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROCESSING
                     PROSITE;
                                                                                                                              ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                               Query Match
                                                                                CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family.
                                                                                                                CHAIN
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                                                                                                                                                                                                                         Matches
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InterPro; IPR002398; ICE.
InterPro; IPR002398; ICE.
InterPro; IPR001318; ICE.p10.
InterPro; IPR001309; ICE.p20.
Pfam; PF00655; ICE.p10; 1.
Pfam; PF00656; ICE.p20; 1.
PRINTS; PR001376; ILLBCENZYME.
PROSITE; PS01122; CASPASE_LYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P10; 1.
Hydrolase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
1-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Gastrula zinc finger protein XLCGF71.1 (Fragment).
Excepts laevis (African clawed frog).
Eukaryota; Metazoa; Chordeta; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred, No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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BY SIMILARITY.

MISSING (IN ISOFORM BETA).

BD9204E23CE1F670 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CASPASE-6 SUBUNIT P18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CASPASE-6 SUBUNIT P11.
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  "CDNA cloning and expression of rat and human protein geranylgeranyltransferase type-I."; J. B10.1 Chen. 269:3175-3180(1994).
-!- FUNCTION: CATALYZES THE TRANSER OF A GERANYL-GERANYL MOIETY FROM GERANYLGERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL SEQUENCE CYS-ALIPHATIC-ALIPHATIC-X. ACTS ON THE RAC1, RAC2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAPIA AND RAPIB PROTEINS.
COPCACUPE. BINDS ONE ZINC ION (BY SIMILARITY).
SUBUNIT: HETERODIMER OF THE AND A BETA SUBUNIT.
SIMILARITY: BELONGS TO THE PROTEIN PRENYLIRANSFERASE BETA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                Gaps
                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Geranylgeranyl transferase type I beta subunit (EC 2.5.1.-) (Type protein geranyl-gerangltransferase beta subunit) (GGTase-Irbeta).
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 377;
15;
   Length 140;
                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFTB 1.
PFTB 2.
PFTB 4.
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
W; 565CD9B6C087A4DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Placenta, and Kidney;
MEDLINE-94148804; PubMed-8106351;
Shang F.L., Diehl R.E., Kohl N.E., Gibbs J.B., Giros Casey P.J., Omer C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;;
Score 30; DB 1;
Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prenyltransferase; Repeat; Zinc.
                                                                                                                                                             377 AA
                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i - SIMILARITY: CONTAINS 4 PFTB REPEATS.
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Pred. No.
                                                                                                                                                                PRT;
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Pfam; PF00432; prenyltrans; 5.
Transferase; Prenyltransferase: Re
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                                                                                                                                                                                             Created)
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85.7%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L25441; AAA35888.1; -. Genew; HGNC:8895; PGGT1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.7%;
85.7%;
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                             6; Conservative
                                                                                                                                                                STANDARD;
                                                                                                                                                                                           01-OCT-1996 (Rel. 34,
                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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377 AA;
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|7 DRSHLTR 23
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Best Local Similarity
Matches 6; Conserv
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              Best Local Similarity
Matches 6; Conserv
                                                           1 DRSNLTR 7
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 602031;
                                                                                                                                                            PGT1_HUMAN
P53609;
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Query Match
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REPEAT
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                          -i- FUNCTION: IMPORTANT DETERMINANT OF VIRUS INFECTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                        Guinea pig cytomegalovirus (strain 22122 / ATCC VR682) (GPCMV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Muromegalovirus.
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Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                      MEDINE-88187294; Pubmed-9526546;
Brady R.C., Schleiss M.R.;
"Identification and characterization of the guinea-pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13E0424C81FCCA16 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yiiQ precursor.
                            (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC
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GLYCOPROTEIN H.
POTENTIAL.
722 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 33; ive 0; Mismatches
                                                                                                                                                                                                                 cytomegalovirus glycoprotein H gene.";
Arch. Virol. 141:2409-2424(1996).
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR003493; Herpes_glycopH.
Pfam; PF02489; Herpes_glycop_H; 1.
Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81609 MW;
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U49361; AAC56576.1; -.
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                                                                   Glycoprotein H precursor.
GH OR UL75.
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| DRSNLT 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               722 AA;
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                                                                                                                                  NCBI_TaxID-103920;
                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                         15-DEC-1998
15-DEC-1998
16-OCT-2001
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                                                                              UL75.
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P32160;
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CARBOHYD
CARBOHYD
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Matches
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                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The genes responsible for O-antigen synthesis of Vibrio cholerae 0139 are closely related to those of Vibrio cholerae 022."; Gene 237:321-332(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dumontier S.E., Escuyer V.E., Berche P.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: GDP-mannose = GDP-4-dehydro-6-deoxy-D-mannose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-MO45 / ATCC 51394 / Serotype 0139;
MEDLINE-99453293; Pubmed-10521656;
Yamasaki S., Shimizu T., Hoshino K., Ho S.-T., Shimada T., Nair G.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
               MEDLINE-93347969; PubMed-8346018;
Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
"Analysis of the Escherichia coli genome. III. DNA sequence of the
region from 87.2 to 89.2 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable GDP-mannose 4,6-dehydratase (EC 4.2.1.47) (GDP-D-mannose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- COFACTOR: NAD(+).
-1- PATHWAY: Conversion of GDP-mannose to GDP-fucose; first step.
-1- SIMILARITY: BELONGS TO THE GDP-MANNOSE 4,6-DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-AI-1837 / Serotype 0139;
MEDLINE-97252505; PubMed-9098074;
Stroeher U.H., Parasivam G., Dredge B.K., Manning P.A.;
Novel Vibrio cholerae 0139 genes involved in lipopolysaccharide blosynthesis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL PROTEIN YILQ. C946DA941973F334 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 29; DB Pred. No. 13; 2; Mismatches
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STRAIN-MO45 / ATCC 51394 / Serotype 0139;
                                                                                                         Nucleic Acids Res. 21:3391-3398(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 179:2740-2747(1997).
                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000466; AAC76902.1; -. PIR; S40863; S40863. EcoGene; EG11874; yilQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21763 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 82.9%;
Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                               EMBL; L19201; AAB03052.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 1
199 AA;
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73 DKANLTR 79
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Q56598;
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                             between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email.to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stevenson G., Andrianopoulos K., Hobbs M., Reeves P.R.;
"Organization of the Escherichia coli K-12 gene cluster responsible for production of the extracellular polysaccharide colanic acid.";
J. Bacteriol. 178:4885-4893(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-KIZ. / MG1657.
STRAIN-KIZ. / MG1657.
PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR001509; Epimerase_Dh.
Pfam; PF01370; Epimerase; 1.
Lipopolysaccharide biosynthesis; Lyase; NAD.
SEQUENCE 372 AA; 41992 MW; 11762663764B3E57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 29; DB 1;
Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12;
MEDLINE=96326333; PubMed=8759852;
                                                                                                                                                                                                                                                                          EMBL; Y07786; CAA69111.1; -. EMBL; AB012956; BAA33595.1;
                                                                                                                                                                                                                                                                                                                                                   EMBL; U24571; AAA77032.1;
HSSP; P32054; 1DB3.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                  Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Schoplete genome sequence of enterohemorrhagic Escherichia coli "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Somoza J.R., Menon S., Schmidt H., Joseph-McCarthy D., Dessen A., Stahl M.L., Somers W.S., Sullivan F.X.;

"Structural and kinetic analysis of Escherichia coll GDP-mannose 4,6 dehydratase provides insights into the enzyme's catalytic mechanism and regulation by GDP-fucose.";

Structure 8:123-135(2000).

-I- CATALYTIC ACTIVITY: GDP-mannose = GDP-4-dehydro-6-deoxy-D-mannose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- COFACTOR: NADP(+).
-i- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF THE SLIME POLYSACCHARIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLANIC ACID. FIRST OF THE THREE STEPS IN THE BIOSYNTHESIS OF GDP-FUCOSE FROM GDP-MANNOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sturla L., Bisso A., Zanardi D., Benatti U., de Flora A., Tonetti M., "Expression, purification and characterization of GDP-D-mannose 4,6-dehydratase from Escherlind coli."; FEBS Lett. 412:126-130(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aoyama K., Haase A.M., Reeves P.R.;
"Evidence for effect of random genetic drift on G+C content after
lateral transfer of fuccose pathway genes to Escherichia coli K-12.";
Mol. Biol. Evol. 11:829-838(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SIMILARITY: BELONGS TO THE GDP-MANNOSE 4,6-DEHYDRATASE FAMILY.
                                                                                                                                                                                                            "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
SEQUENCE FROM N.A.

STRAIN-0157.H7 / EDL933 / ATCC 700927;

MEDLINE-21074935. PubMed-1120651;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Lin A., Shador Y., Miller L.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EcoGene; EG11787; gmd.
InterPro; IPR001509; Epimerase_Dh.
Pfam; PF01370; Epimerase; 1.
Lipopolysaccharide biosynthesis; Lyase; NADP; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
                                                                                                                                                                                                                                                                                                  STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20139699; PubMed-10673432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97400210; PubMed-9257704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95115532; PubMed-7815923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE000295; AAC75114.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D90843; BAA15909.1; -.
EMBL; AE005431; AAG57113.1; -.
EMBL; AP002559; BAB36281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 50-373 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U38473; AAC77842.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1DB3; 24-NOV-99.
                                                                                                                                                                                                                                                          [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K]
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                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=El Tor N16961 / Serctype Ol;
STRAIN=El Tor N16961 / Serctype Ol;
MEDLINE=20406833; PubMed=10952301;
Meidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406:477-483(2000).
-!- CATALYTIC ACTIVITY: GDP-mannose = GDP-4-dehydro-6-deoxy-D-mannose
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Conversion of GDP-mannose to GDP-fucose; first step.
-!- SIMILARITY: BELONGS TO THE GDP-MANNOSE 4,6-DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
LoCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last amoctation update)
Probable GDP-mannose 4,6-dehydratase (EC 4.2.1.47) (GDP-D-mannose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEROISCE FROM N.A.
SEROISCE TO O.17 / Serotype 01;
MEDLINE-95309704; PubMed-7540582;
Manning P.A., Stroeher U.H., Karageorgos L.E., Morona R.;
Putative O-antigen transport genes within the rfb region of cholerae of are homologous to those for capsule transport."
                                                                  Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stroeher U.H., Karageorgos L.E., Morona R., Manning P.A.; "Serotype conversion in Vibrio cholerae Ol."; Proc. Natl. Acad. Sci. U.S.A. 89:2566-2570(1992).
                                                                                                   Indels
                                 1A9BA2A7C566DE11 CRC64;
                                                                  DB 1;
26;
                                                                                                                                                                                                                                                       373 AA
                                                                                                  0; Mismatches
                                                                  Score 29;
                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: NAD(+) (BY SIMILARITY).
                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-E1 Tor O17 / Serotype O1;
MEDLINE-92212870; PubMed-1372980;
                              373 AA; 42047 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X59554; CAA42136.1; -.
EMBL; AE004113; AAF93419.1; -.
HSSP; P32054; 1DB3.
TIGR: VC0243; -.
                                                                  82.9%;
                                                                                                     Conservative
                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                             dehydratase).
RFBD OR GMD OR VC0243.
                                                                                                                                                                     67 DISNLTR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 158:1-7(1995).
                                                                Query Match
Best Local Similarity
                                                                                                                                     1 DRSNLTR 7
                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     + H(2)0
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9
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Q06952;
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Complete pact_SITE SEQUENCE
                                                                                                                                                                                                                       RESULT 9
GMD1_VIBCH
                                                                                                   Matches
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DRSNLDR 92
                         98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
                                                                                      RESULT 11
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@liber.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Geranylgeranyl transferase type I beta subunit (EC 2.5.1..) (Type I
protein geranyl-geranyltransferase beta subunit) (GGTase-I-beta).
PGGTIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94148804; PubMed-8106351;
Zhang F.L., Diehl R.E., Kohl N.E., Gibbs J.B., Giros B.,
Zhang F.L., Diehl R.E., Kohl N.E., Gibbs J.B., Giros B.,
Zhang F.L., Diehl R.E., Kohl N.E., Gibbs J.B., Giros B.,

"Casay P.J., Omer. C.A.,

"CDNA cloning and expression of rat and human protein
geranylgeranyltransferase type-I.";
J. Biol. Chem. 259:3175-3180(1994).

"I FUNCTION: CATALIZES THE TRANSFER OF A GERANYL-GERANYL WOIETY FR
GERANYLGERANYL PYROPHOSPHATE TO PROTEINS HAVING THE C-TERMINAL
SEQUENCE CYS-ALIPHATIC-ALIPHATIC-X. ACTS ON THE RACI, RAC2,
                 Pfam; PF01370; Epimerase; 1.
Lipopolysaccharide blosynthesis; Lyase; NAD; Complete proteome.
SEOUENCE 373 AA; 42053 MW; 4EB10DCAB6A8C1D2 CRC64;
                                                                                                                                                   ö
                                                                                                     Score 29; DB 1; Length 373;
Pred. No. 26;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 377;
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INC (BY SIMILARITY).
AADEC7301A4A4011 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prenyltransferase; Repeat; Zinc.
                                                                                                                                                                                                                                                                                                                                      377 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - SIMILARITY: CONTAINS 4 PFTB REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFTB 2.
PFTB 3.
PFTB 4.
ZINC (BY SZINC (BY SZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFTB 1
InterPro; IPR001509; Epimerase_Dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR001330; Prenyltrans.
Pfam; PF00432; prenyltrans; 5.
Transferase; Prenyltransferase; Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42414 MW;
                                                                                                   82.9%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.9%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L24116; AAA17756.1; -.
                                                                                                                           Similarity 85.7
6; Conservative
                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                                DSSNLTR 74
                                                                                                                                                                                         DRSNLTR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                  PGT1_RAT
P53610;
                                                                                                         Query Match
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                                                                                                                             Local
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                             10
                                                                                                                                            Matches
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    SKRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1 - COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L19511; AAA67850.1; -.
InterPro; IPR000179; Cyt_b_b6.
Pfam; PF00032; cytochrome_b_c; 1.
Pfam; PF00033; cytochrome_b_n; 1.
PROSITE; PS00192; CYTOCHROME_B.HEME; 1.
PROSITE; PS00193; CYTOCHROME_B.O0; 1.
Mitochondrion; Electron transport; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  den Bussche R.A., Hudgeons J.L., Baker R.J.; "Phylogenetic accuracy, stability, and congruence: relationships within and among the New World bat genera Artibeus, Dermanura, and
                                                                                                                                                                                             Artibeus cinereus (Gervais' fruit-eating bat) (Dermanura cinerea).
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
Stenodermatinae; Artibeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOUND TO THE PROTEIN.
--- SUBUNTT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN.
--- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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IRON 2 (HEME B566 AXIAL LIGAND).
IRON 2 (HEME B562 AXIAL LIGAND).
IRON 1 (HEME B566 AXIAL LIGAND).
I -> V (IN REF. 2).
8E90A6FF5E2D3DE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29; DB 1; Length 379; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koopmania.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
CYB_ARTCI STANDARD; PRT; 3/9 AA. 055726; 034305; Teated) 15-JUL-1999 (Rel. 38, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-TK 18790 / AMNH 267197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42697 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U66511; AAB06766.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.9%;
ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-134 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
97
182
196
                                                                                                                                                                 MICYB OR COB OR CYTB.
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-40224;
                                                                                                                                        Cytochrome B.
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Gaps

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1; Indels

0; Mismatches

6; Conservative

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Query Match
                                                                                    ZN_FING
ZN_FING
ZN_FING
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ZN_FING
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                                                                                                                                                                                                                       ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 629-810 FROM N.A.

SEQUENCE OF 629-810 FROM N.A.

MEDLINE-921319; PubMed-8464732;

A Tunnacliffe A., Liu L., Moore J.K., Leversha M.A., Jackson M.S.,

A Ferguson-Smith M.A., Thiesen H.-J., Ponder B.A.;

Tunplicated Kox zinc finger gene clusters flank the centromere of human chromosome 10: evidence for a pericentric inversion during primate evolution.;

I Nucleic Acids Res. 21:1409-1417(1993).

C -! SUBCELULAR LOCATION: Nuclear (Potential).

-! SINICALIY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.

C -! SIMILARITY: CONTAINS 1 KRAB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Bone marrow;
MEDLINE-96051398; PubMed=7584044;
Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.;
Frediction of the coding sequences of unidentified human genes. II.
The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by analysis of CDNA clones from human cell line KG-I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 16.
SMOSITE; PS50805; KRAB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 16.
PROSITE; PS0107; ZINC_FINGER_C2H2_2; 16.
Transcription regulation; Zinc-finger; DNA-binding; Metal-binding;
                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
2inc finger protein 33A (Zinc finger protein KOX31) (HA0946).
ZNF33A OR ZNF33 OR KOX31 OR KIAA0065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSFAC, T04984; -. Genew, HGNC:13096; ZNF33A. InterPro; IPR001909; RRAB. InterPro; IPR00082; Znf_C242. Pfam; PF00096; Zf_C242; 16. Pfam; PF01352; KRAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00048; ZINCFINGER.
ProDom; PD000003; Znf_C2H2; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D31763; BAA06541.1; -. EMBL; X68687; CAA48646.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X68689; CAA48648.1; -.
                                                                                                                                                     STANDARD;
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DOMAIN

12

83

ZN_FING

ZN_FING

356

378
                                         171 DKANLTR 177
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  DRSNLTR 7
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                     233A_HUMAN
Q06730;
                                                                                                         RESULT 12
Z33A_HUMAN
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                                                                                                                                                                                                                                                                                                                           Gaps
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25 X 9 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Gehrung S., Snyder M.;
The SPA2 gene of Saccharomyces cerevisiae is important for
Pheromone-induced morphogenesis and efficient mating.";
J. Cell Biol. 111:1451-1464(1990).
                                                                                                                                                                                                                                                                                     Length 810;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                  96AD969EF541B73E CRC64;
                                                                                                                                                                                                                                                                                     DB 1;
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01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1466 AA
                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                      64;
                               C2H2-TYPE.
                                                                                                                                                                                                                                                                                       Score 29;
                                                                                                                                                                                                                                   C2H2-TYPE
                                                                                                                                                                                                                                                                                                          Pred. No.
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SPA2 OR PEA1 OR YLL021W OR L1209.
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SGD; SO003944; SPA2.
Cell shape; Repeat; Coiled coil.
DOMAIN 818 COI
DOMAIN 818 1087 25
                                                                                                                                                                                                                                                    94384 MW;
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367 DKSNLTK 373
                                                                                                                                                                                                                                                  810 AA;
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Matches 5; Conserv
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STRAIN-S288c;
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SEQUENCE
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Tree precursor...;

Tree precursor...;

Tree precursor...;

Tree precursor...;

Tree precursor...;

Tree precursor...;

Tree processive and precursor...;

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Tree processive 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATCC 27064 / DSM 738 / NRRL 3585;
STRAIN-ATCC 27064 / DSM 738 / NRRL 3585;
MEDLINE-92325051; Pubmed-1339424;
Ludovice M., Martin J.F., Carrachas P., Liras P.;
Characterization of the Streptomyces clavuligerus argC gene encoding N-acetyjdlutemyl-phosphate reductase: expression in Streptomyces 11vidans and effect on clavulinic acid production.";
J. Bacteriol. 174:4606-4613(1992).
-I- CATALTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
AMIDATION (G-10 PROVIDE AMIDE GROUP).
N-LINKED (GLCNAC...).
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01-007-1996 (Rel. 34, Last sequence update)
15-7UN-2002 (Rel. 41, Last annotation update)
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-acetyl-glutamate semialdehyde dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobactéria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomyclneae; Streptomycetaceae; Streptomyces. NCBI_TaxID=1901;
         MEDLINE-86136563; PubMed-3081370;
Chauvet M.-T., Chauvet J., Acher R.;
"Guinea pig copeptin. The glycopeptide domain of the vasopressin precursor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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15;
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CE2B18A162C9ABEA CRC64;
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Pred. No. 15;
2; Mismatches
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71.4%;
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Best Local Similarity
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MEDLINE-87247214; PubMed=3595848;
Chauvet J., Chauvet M.-T., Acher R.;
"Conformation limited proteolysis in the common neurophysin-copeptin precursor shown by trypsin-sepharose chromatographic proteolysis.";
FEBS Lett. 217:180-183(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-88138574; PubMed-3436704;
Chauvet M.-T., Chauvet J., Acher R.;
"Guinea pig MSEL-neurophysin. Sequence comparison of eight mammalian
MSEL-neurophysins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chauvet M.-T., Rouille Y., Chauvet J., Acher R.; "Guinea pig neurohypophysial hormones. Peculiar processing of the three-domain vasopressin precursor.";
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01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vasopressin neurophysin 2-copeptin precursor [Contains: Arg-vasopressin; Neurophysin 2 (Neurophysin-II); Copeptin].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1466;
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..3e+02;
... 1; Indels
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25.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
MW; 2EBB616152382C89 CRC64;
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Pred. No. 1.3e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 85.7 nes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1045
1054
1072
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1169
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1466
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P10769;
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+ phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
-!- PATHWAY: Arginine biosynthesis; third step.
-!- SIMILARITY: BELONGS TO THE NAGSA DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 80.0%; Score 28; DB 1; Length 340; Best Local Similarity 71.4%; Pred. No. 40; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BC270C115D9B494F CRC64;
                                                                                                                                                                                                                                                          EMBL; M83659; AAA26704.1; -.
InterPro; IPR000706; AGPR_act_site.
InterPro; IPR000534; Semialdh_dh.
Pfam; PF021118; Semialdhyde_dh; 1.
Pfam; PF02774; Semialdhyde_dhc; 1.
ProDom; PD003765; AGPR_act_site; 1.
PROSITE; PS01224; ARGC; 1.
Arginine biosynthesis; Oxidoreductase; NADP. ACT_SITE 145 BY SIMILARITY.
SEQUENCE 340 AA; 35299 MW; BC270C115D98494F
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Job time: 7.66667 secs
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303 DRDNLTK 309
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 15, 2003, 12:50:16; Search time 23.6667 Seconds Run on:

(without alignments)
60.944 Million cell updates/sec

US-10-006-069A-55 35 1 DRSNLTR 7 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp_archea:* sp_bacteria:* SPTREMBL_21:*

sp_vertebrate:*
sp_unclassified:* sp_fungi:*
sp_human:*
sp_invertebrate:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_organelle:* sp_phage:* sp_rodent:* sp_mammal:* sp_plant:* sp_virus:* sp_mhc:* 10: 111: 12: 14:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Q8rnn1 legionella
1D 095213 090213 090089 090089 090087 09087 091077 091077 090874 09851 09851	QBRNNI
DB 110 111 111 113 113 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	~
Match Length, DB  Match Length, DB  11.4 530, 16  88.6 276 11  88.6 276 11  88.6 293 4  88.6 1941 13  88.6 1941 13  88.7 182 2  85.7 294 4  85.7 292 4  85.7 321 2  85.7 321 2	413
Match Match 11.4 88.6 88.6 88.6 88.6 88.6 88.7 85.7 85.7 85.7	85.7
8 31 31 31 31 31 31 31 31 31 31 31 31 31	30
Result No. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	۹٦

095363 homo sapien 096397 brachydanio 075094 homo sapien 088280 rattus norv 09wvb4 mus musculu 094040 oncorhynchu 08273 salmonella 08273 salmonella 09822 rhizobium 1030416 lactococcus 099218 lactococcus 099292 streptomyce 05659 vibrio chol 094077 clethrionom 094073 salmonella 093433 salmonella	Q95522 escherichia 08539 escherichia Q82511 salmonella Q9f7a4 salmonella Q9f7a4 aeromonas h Q91a94 aeromonas h Q9238 caulobacter Q8573 mus musculu Q9x9w7 streptomyce Q9ug14 homo sapien
4 095363 13 Q9DE37 4 075094 11 0997094 11 0997094 16 082203 16 082273 16 082770 16 09872 2 030416 16 Q9CG18 16 Q9CG18 16 Q9CG59 16 Q9A53 16 Q9A53 16 Q9A53 2 Q5A872 2 Q5A872 2 Q5A872 2 Q5A872	2 095522 16 085339 16 085311 16 09F7A4 2 09LA94 11 09A3R8 11 09R873 16 09X9W7 4 09UG14
1515 1515 1523 1523 16523 16523 1633 1633 1633 1633 1633 1633 1633 16	372 372 373 373 377 381 416 533
88888888888888888888888888888888888888	
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	00000000000000000000000000000000000000
1111 122222222222333333333333333333333	33 33 34 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

SEQUENCE FROM N.A.
SEROTTPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. NCBI_TaxID≈666; 'DNA sequence of both chromosomes of the cholera pathogen Vibrio 01-0CT-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Sigma-54 dependent transcriptional regulator. VCA0182. 530 AA PRT; PRELIMINARY; Q9KMY4; **09KMY4** RESULT 1 Q9KMY4 

Nature 406:477-483(2000). -!- SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING DOMAIN.

ILOKY, VAULOL2;
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR0031018; GAF.
InterPro; IPR0002197; HTH_F1s.
InterPro; IPR002078; Sig54_interact.
Pfam; PF001590; GAF; 1.
Pfam; PF00158; Sigme54_activat; 1.
PRINTS; PR01590; HTHFIS.
SMART; SM00065; GAF; 1. EMBL; AE004358; AAF96095.1; TIGR; VCA0182; -.

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Caspase 6.
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099M47
  DDE READ DR RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/63; TISSUE-SPINAL CORD;

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Coolhwa H.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Coochwa H.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Couckenbush J.,

Sakai K., Okido T., Furuno W., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Ruschincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Ruschin H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Rusching H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Wanshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Rusching V., Wang K., Wang K.H., Weltz C., Wangthy H., Rohtsuki S.,

Rusching V., Wang K., Wang K., Kawaji H., Kohtsuki S.,
              PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
PROSITE; PS00676; SIGMA54_INTERACT_2; 1.
PROSITE; PS00689; SIGMA54_INTERACT_3; 1.
PROSITE; PS50045; SIGMA54_INTERACT_4; 1.
ATP-binding: DNA-binding; Transcription regulation; Complete proteome: SEQUENCE 530 AA; 59026 MW; 5B85E12P25A03FA2 CRC64;
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Adult male spinal cord cDNA, RIKEN full-length enriched library,
clone:A330108A07, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
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0
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EMBL; AKO20743; BAB32198.1; -
SEQUENCE 241 AA; 27834 MW; 53E65B634A3C9609 CRC64;
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Last annotation update)
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                          Query Match
Best Local Similarity 85.7.
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Best Local Similarity 85.77
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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TIGREAMS; TIGR01199;
                                                                                                                                                                                                                                                                                                                        505 DRANLTR 511
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                                                                                                                                                                                                                                                                            1 DRSNLTR 7
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01-JUN-2001
01-JUN-2002
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O9D213;
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A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Alzawa T., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Saito T., Saito T., Saito R., Kuchi P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H., Kuchi P., Lewis S., Matsuo Y., Nikaido I., Rasha B., Kochiwa H., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., Kaniya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., M., Wandani R., Wandani R., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Functional annotation of a full-length mouse cDNA collection.";
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10 days embryo cDNA, RIKEN full-length enriched library, clone:2610037G10, full insert sequence.
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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0; Mismatches
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SMUOLLD; CMBC, TORSPARE, CYS; PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_HIS; PROSITE; PS50208; CASPASE_P20; PROSITE; PS50208; CASPASE_P20; CROTHENCE 276 AA; 31591 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1312921; Casp6.
InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
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Pfam; PF00656; ICE_D20; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
EMBL; AK011710; BAB27792.1;
HSSP; P42574; 1PAU.
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85.7%;
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Best Local Similarity 85.7.,
6; Conservative
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                                                                                                                                                                                                   NCBI_TaxID-10090;
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us-10-006-069a|-55.rspt

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01-MAY-1997 (
01-MAY-1997 (
01-DEC-2001 (
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P79793;
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Q8UWA0
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                   88.6%; Score 31; DB 11; Length 276; 85.7%; Pred. No. 40;
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85.7%; Pred. No. 43;
ive 0; Mismatches 1; Indels
                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
EMBL; BCO04460; AAH04460.1; -.
EMBL; BCO00305; AAH00305.1; -.
                                                                                                                                5965C5932A127B6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 AA; 33310 MW; 0738AE4F9791EBD7 CRC64;
                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Caspase 6, apoptosis-related cysteine protease.
                                                                                                                                                                                                                                                         293 AA
                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                         PRT;
                                                                                         PROSITE; PSO1122; CASPASE_CYS; 1. PROSITE; PSO1121; CASPASE_HIS; 1. PROSITE; PS550207; CASPASE_PIO; 1. PROSITE; PS50208; CASPASE_PSO; 1. SEQUENCE 276 AA; 31363 MW; 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01122; CASPASE_CYS; 1. PROSITE; PS01121; CASPASE_HIS; 1. PROSITE; PS50207; CASPASE_PIO; 1. PROSITE; PS50208; CASPASE_PS0; 1.
      HSSP, P42574; 1PAU.

MGD: MGI:131221; Casp6.

InterPro: IPR002139; ICE.

InterPro: IPR002139; ICE_D10.

InterPro: IPR001309; ICE_D20.

Pfam; PF00655; ICE_D10; 1.

Pfam; PF00656; ICE_D20; 1.

Pfam; PR00576; ILLBCENZYRE.

SWART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
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Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
BC002022; AAH02022.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.,
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                  || || || 53 DRDNLTR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || |||||
70 DRDNLTR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P42574; 1PAU.
                                                                                                                                                  Ouery Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                       1 DRSNLTR 7
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE=LUNG;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; C14.005;
                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protease.
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Q9BQE7;
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SEQUENCE FROM N.A.

Machida S., Noda S., Takao A., Momma K., Matsuoka R.;

Machida S., Noda S., Takao A., Momma K., Matsuoka R.;

"Defferential expression of chick slow skeletal myosin heavy chains in
the developing Purkinje myozytes.";

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AB057661; BAR79445.1;

InterPro; IPR000048; IQ_region.

InterPro; IPR001609; Myosin_head.

InterPro; IPR001928; Myosin_head.

InterPro; IPR001928; Myosin_tail.

InterPro; IPR00159; SHprot_acsite.

Pfam; PF00612; IQ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                          SECTENCE FROM N.A. STRAIN-WHITE LEGHORN; TISSUE-LEG MUSCLE; Chen Q., Moore L.A., Wick M., Bandman E.; "Identification of a genomic locus containing three slow myosin heavy
                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=WHITE LEGIORN; TISSUB=LEG MUSCLE;
Chen Q., Moore L.A., Zhang J., Bumstead N., Bandman E.;
Chen Q., Moore L.A., Zhang J., Bumstead N., Bandman E.;
chen Q., Moore L.A., Chang J., Bumstead N., Bandman E.;
submitted different loci.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U85023; AAB41890.1;
InterPro; IPR002328; Myosin_tail.
InterPro; IPR00533; Tropomyosin.
Pfam; PF01576; Myosin_tail: 1.
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88.6%; Score 31; DB 13; Length 761;
Best Local Similarity 85.7%; Pred: No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain genes.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 761 AA; 88289 MW; A8538787E29E3B46 CRC64;
                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
761 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1941 AA
                                                                                       01-MAY-1997 (TrEMBLrel. 03, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
Slow myosin heavy chain 2 (Fragment)
                                                         03, Created)
03, Last sequ
PRT;
PRELIMINARY;
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                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || ||||
685 DRKNLTR 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin heavy chain.
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NCBI_TaxID=9606;
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STRAIN=2241 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=2022556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Erown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moules S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                Score 31; DB 13; Length 1941;
Pred. No. 2.9e+02;
0; Mismatches 1; Indels
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                Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_Lali; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; MYOSINHEAVY.
SMART; SM0242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
PROSITE; PS600639; THIOL_PROTEASE_HIS; UNKNOWN_1.
SEQUENCE 1941 AA; 224292 MW; 96B2D8890E148D4D CRC64;
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EMBL; AL162752; CAB83381.1; -
InterPro; IPR002106; AAtRNA_LigaseII.

Lipoprotein; Complete protecome.

ELIPOPROTEIN: COMPLETE PROMELIESE II_2; UNKNOWN_I.

ELIPOPROTEIN: Complete protecome.

SEQUENCE 125 AA; 13888 MW; A20C7C09F48081E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Hypothetical 21.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
Pfam; PF00063; myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                         Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                   1865 DRKNLTR 1871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative lipoprotein.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                     Query Match
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Q9RBT4
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096644;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Unknown (protein for MGC:16594).
Homo saplens (Human).
Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DJ520B18.2 (FARSI (Phenylalanine-tRNA synthetase)) (Fragment)
                                                                                                                                                                           Query Match 85.7%; Score 30; DB 2; Length 182; Best Local Similarity 85.7%; Pred. No. 45; Matches 6; Conservative 1; Mismatches 0; Indels
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EMBL; AL121978; CAC00668.1; -.
HSSP; P27001; 1PYS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 204 AA; 23516 MW; 4DC8AF7BF7FD17B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002106; AATRNA_ligaseII.
Interpro; IPR002319; tRNA-synt_2d.
Pfam: PF01409; tRNA-synt_2d; 1.
PROSITE; PS00179; AA_TRNA_LIGASE_II_1; UNKNOWN_1.
Aminoacy1-tRNA synthetase:
NON_IER 204 204 204
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34 DRSSLTR 40
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Best Local Similarity
                                                                                                                                                                                                                                                                      1 DRSNLTR 7
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TISSUE-MUSCLE;
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Nakayama J., Yoshida K., Kobayashi H., Isogai A., Clewell D.
                                                                                                                                                                                                                                                                                                                              Plasmid pPD1
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                                                                                         SEQUENCE
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Q52195
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Q9UMC5
ID Q9UMC
DT 01-MA
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DT 01-JU
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InterPro; IPR000822; Znf_C2H2.

InterPro; IPR000862; Znf_C2H2.

PRIMTS; PR00048; ZINCTRUER.

Probom; PD000003; Znf_C2H2; 6.

SMART; SM00355; Znr_C2H2; 9.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 8.

PROSITE; PS50157; ZINC_FINGER_C2H2_1; 9.

DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein; Zno-finger.
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Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 33.5 kDa protein.
Hypothetical Butheria, Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 73;
1; Mismatches 0; Indels
                                                                            Query Match 85.7%; Score 30; DB 4; Length 292; Best Local Similarity 85.7%; Pred. No. 73; Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLIAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; BC005068; AAH05068.1;
          Prodom; PD000003; Znf_C2H2; 6.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_8.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 9.
DNA-binding; Zinc_finger.
SEQUENCE 292 AA; 33497 MW; 3A5E633635C36385 CRC64;
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Last sequence update)
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MEDLINE=96032393; PubMed=7559344;
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85:7%;
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Pfam; PF00096; zf-C2H2; 9.
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6; Conservative
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                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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Q9BSG1
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"Cloning and characterization of a region of enterococcus faecalis plasmid pPD1 encoding pheromone inhibitor (ipd), pheromone sensitivity (trac), and pheromone shutdown (traB) genes.";

EMBL; D28859; BAA06009.1;

Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96032394; PubMed-7559345; Fujimoto K., Ike Y.; Fujimoto S., Tomita H., Wakamatsu E., Tanimoto K., Ike Y.; Physical Mapping of the Conjugative Bacteriocin Plasmid pPD1 of Enterococcus faecalis and Identification of the Determinant Related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of a region of enterococcus faecalis plasmid pPD1 encoding pheromone inhibitor (ipd), pheromone sensitivity (trac), and pheromone shutdown (traB) genes."; J. Bacteriol. 177:5567-5573(1995).
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MEDLINE-96032393; PubMed-7559344;
Nakayama J., Yoshida K., Kobayashi H., Isogai A., Clewell D.,
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Last sequence update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
2.1 finger 2.2 (Fragment).
2.NF2.2.
Homo sapiens (Human).
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81;
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100.0%; Pred. No. 81;
ive 0; Mismatches
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J. Bacteriol. 177:5574-5581(1995).
EMBL; D78016; BAA11197.1; -.
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NCBI_TaxID=1351;
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01-NOV-1996 (TrEMBLrel. 01,
01-JAN-1999 (TrEMBLrel. 09,
                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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Search completed: July 15, 2003, 12:54:47 Job time: 25.6667 secs

111:111 271 DRSSLTR 277

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GenCore version 5.1.6

Copyright,(c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 12:53:06; Search time 16.3333 Seconds

(without alignments)

49.894 Million cell updates/sec

Title: US-10-006-069A-55

Perfect score: 35
Sequence: 1 DRSNLTR 7

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5
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Total number of hits satisfying chosen parameters: 445758

445758 segs, 116419773 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		,				
· Result		* Query				
No.	Score	Match	Length DB	88	QI	Description
-	35	100.0	7	σ	US-10-006-069A-36	Sequence 36, Appl
7	35	100.0	7	6	US-10-006-069A-55	55,
m	35	100.0	7	σ	US-10-006-069A-56	56,
4	35	100.0	7	6	US-10-006-069A-59	59,
ហ	35	100.0	7	6	US-10-006-069A-67	, 79
9	35	100.0	7	δ	US-10-006-069A-134	134,
7	35	100.0	7	σ	US-10-006-069A-167	Sequence 167, App
80	35	100.0	7	6	US-10-006-069A-170	Sequence 170, App
6	35	100.0	7	6	US-10-006-069A-196	196,
10	35	100.0	7	σ	US-10-006-069A-198	198,
11	35	100.0	7	σ	US-09-846-033B-36	36,
12	35	100.0	7	σ	US-09-846-033B-55	Sequence 55, Appl
13	35	100.0	7	σ	US-09-846-033B-56	Sequence 56, Appl
14	35	100.0	7	6	US-09-846-033B-59	Sequence 59, Appl
15	35	100.0	7	6	US-09-846-033B-67	Sequence 67, Appl
16	35	100.0	7	σ	US-09-846-033B-134	Sequence 134, App
17	35	100.0	7	σ	US-09-846-033B-167	Sequence 167, App
18	35	100.0	7	6	US-09-846-033B-170	Sequence 170, App
19	32	100.0	7	σ	US-09-846-033B-196	Sequence 196, App

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0; Gaps

1 DRSNLTR 7 ||||||| 1 DRSNLTR 7

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Sequence 198, App Sequence 37, Appl Sequence 395, App	1454, 1454, 1464, 1525,	1559, 1564, 1577,			3006, 3131, 3197, 3216,
7 9 US-09-846-033B-198 7 9 US-00-055-713-37 7 9 US-0990-186-395 7 0 ITC-00-000-186-1376	-09-990-186-14 -09-990-186-14 -09-990-186-14 -09-990-186-15	US-09-990-186-1 US-09-990-186-1 US-09-990-186-1	7 9 US-0990-186-1899 7 9 US-09-990-186-2668 7 9 US-09-990-186-2705 7 9 US-0990-186-2737 7 9 US-09-990-186-2731	US-09-990-186- US-09-990-186- US-09-990-186- US-09-990-186-	-09-990-186- -09-990-186- -09-990-186- -09-990-186-
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## ALIGNMENTS

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US-10-006-069A-36

| Sequence 36, Application US/10006069A
| Sequence 36, Application Sequence 36, Applicant Belant Sequence 36, Applicant Liu, Pel-0i
| APPLICANT: Liu, Pel-0i
| APPLICANT: Wolffe, Alan | APPLICANT: Standamo BioSciences, Inc. | APPLICANT: Standamo BioScience, Inc. | APPLICANT: Standamo BioScience, Inc. | APPLICANT: Standamo BioScience | APPLICANT: Standamo BioScience | APPLICANT: | APPLICANT
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APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Qi
APPLICANT: Holfe, Alan
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
TITLE OF INVENTION: Pinger Proteins
TITLE OF INVENTION: Regulation with Since
TITLE OF INVENTION: Pinger Proteins
TILE REFERENCE: 019496-0058304C
CURRENT APPLICANTON NUMBER: US/10/006,069A
                                                                                                                                           100.0%; Score 35; DB 9; Length 7; 100.0%; Pred. No. 4e+05; Live 0; Mismatches 0; Indels
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100.0%; Score 35; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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APPLICANT: Liu, Ped-Qi
APPLICANT: Liu, Ped-Qi
APPLICANT: Wolffe, Alan
APPLICANT: Jarvis, Eric
APPLICANT: Jarvis, Eric
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-005830US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 59, Application US/10006069A Publication No. US20030021776A1
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APPLICANT: Rebar, Edward APPLICANT: Jamleson, Andrew
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7: Conservative
                                                         ; OTHER INFORMATION: finger US-10-006-069A-56
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1 DRSNLTR 7
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APPLICANT: Jarvis, Etc.
TILE OF INVENTION: Regulation of Anglogenesis With Zinc.
TILLE OF INVENTION: Regulation of Anglogenesis With Zinc.
TILLE OF INVENTION: Regulation of Anglogenesis With Zinc.
TILLE REFERENCE: 019496-005830US
CURRENT APPLICATION NUMBER: US/10/006,069A
CURRENT FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 09/846,033
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 09/846,033
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTHARE: EastSEQ for Windows Version 3.0
SEQ ID NO 55
LENGTH: 7
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APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Olang
APPLICANT: Liu, Pel-Ol
APPLICANT: Liu, Pel-Ol
APPLICANT: Liu, Pel-Ol
APPLICANT: Liu, Pel-Ol
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Fedutation of Angiogenesis With Zinc
CURRENT APPLICATION NUMBER: US/10/006,069A
CURRENT FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SSOFTWARE: FRASED for Windows Version 3.0
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                                                                              Sequence 55, Application US/10006069A Publication Wo. US20030021776A1 GENERAL INFORMATION:
APPLICANT: Rebar, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-10-006-069A-56

: Sequence 56, Application US/10006069A

: Publication Nor US20030021776A1

: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   Wolffe, Alan
Eisenberg, Stephen P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                 Jamleson, Andrew
Liu, Olang
Liu, Pel-Ol
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Best Local Similarity 100.
Matches 7; Conservative
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APPLICANT: Gamieson, Andrew
APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Sangamo BioSciences, Inc.
APPLICANT: Sangamo BioSciences, Inc.
APPLICANT: Sangamo BioSciences, Inc.
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-00830GS
CURRENT APPLICATION NUMBER: US,10/006,069A
CURRENT FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
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SPRIOR FILING DATE: 2000-13-13
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. 46+05;
0; Indels
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                                            PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR PILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-04-30
NUMBER: US 09/846,033
NUMBER: OF SEQ ID NOS: 252
SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
CURRENT APPLICATION NUMBER: US/10/006,069A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 134, Application US/10006069A Publication No. US20030021776A1 GENERAL INFORMATION:
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100.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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; OTHER INFORMATION: finger
US-10-006-069A-134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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Gaps
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              APPLICANT: JOSTA Andrew
APPLICANT: Jangeson, Andrew
APPLICANT: Liu, Olang
APPLICANT: Liu, Dei-Oi
APPLICANT: Wolffe, Alan
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Bangamo BloSciences, Inc.
APPLICANT: Sangamo BloSciences, Inc.
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFRENCE: 019496-006830US
CURRENT APPLICATION NUMBER: US,10/006,069A
CURRENT FILING DATE: 2001-12-17
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APPLICANT: Wolffe, Alan
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Sangamo BioSciences, Inc.
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-005830US
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PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SEQ ID NO 167
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CURRENT FILING DATE: 2001-12-17
PRICE APPLICATION NUMBER: 05 09/733,604
PRICE FILING DATE: 2000-12-07
PRICE APPLICATION NUMBER: US 09/736,083
PRICE FILING DATE: 2000-12-12
PRICE PELICATION NUMBER: US 09/846,033
PRICE PRICE DATE: 2001-04-30
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 170
LEMCTH: 7
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APPLICANT: Rebar, Edward
APPLICANT: Jamleson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-qi
APPLICANT: Wolffe, Alan
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100.0%;
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Best Local Similarity 100.
Matches 7; Conservative
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COTHER INFORMATION: finger
US-10-006-069A-167
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: Rebar, Edward
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100.0%; Score 35; DB 9; Length 7; Best Local Similarity 100.0%; Pred. No. 4e+05; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Elsenberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Jarvis, Eric
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-0058200S
CURRENT APPLICATION NUMBER: US/09/446,033B
CURRENT FILING DATE: 2001-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 9;
Pred. No. 4e+05;
Mismatches 0
             PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 09/846,033
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 198
LENGTH: 7
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PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
PRIOR APPLICATION NUMBER: US 09/736,083
                                                                                                                                                                                                                                               ; OTHER INFORMATION: recognition helix US-10-006-069A-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36, Application US/09846033B Publication No. US/003044404Al GENERAL INFORMATION: AppliCANT: Rebar, Edward APPLICANT: Jamleson, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 55, Application US/09846033B Publication No. US20030044404A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Qi
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu, Qiang
Liu, Pei-Qi
Wolffe, Alan
                                                                                                                                                                                                                                                                                                                                                                                                         1 DRSNLTR 7
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US-09-846-033B-36
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US-09-846-033B-55
                                                                                                                                                                                TYPE: PRT
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GREATLION:
APPLICANT: Rebar, Edward
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Qi
APPLICANT: Liu, Pei-Qi
APPLICANT: Liu, Pei-Qi
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc
FILE REFERENCE: 019496-0058300S
CURRENT FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2001-12-17
PRIOR PELING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 196
                  DB 9; Length 7; 4e+05;
                                                              0; Indels
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APPLICANT: Liu, Pei-Oi
APPLICANT: Wolffe, Alan
APPLICANT: Wolffe, Alan
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Sangamo BloSciences, Inc.
TITLE OF INVENTION: Requilation of Angiogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-005830US
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100.0%; Pred. No. 4e+05;
iive 0; Mismatches 0;
                                                                 Mismatches
                  100.0%; Score 35; 100.0%; Pred. No.
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PRIOR EPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                               Sequence 196, Application US/10006069A Publication No. US20030021776A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 198, Application US/10006069A Publication No. US20030021776A1 GENERAL INFORMATION: APPLICANT: Rebar, Edward APPLICANT: Jamieson, Andrew
                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
             Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
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US-10-006-069A-198
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Sequence 57, Application US/09846033B
Sublication No. US20030044404A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bebar, Edward
APPLICANT: Liu, Olang
APPLICANT: Liu, Pel-Q1
APPLICANT: Liu, Pel-Q1
APPLICANT: Liu, Pel-Q1
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Sendeng Stephen P.
APPLICANT: Sendeng Stephen P.
APPLICANT: Sendeng BioSciences, Inc.
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc;
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc;
TITLE OF INVENTION: Ringer Proteins
FILE REFERENCE: 019496-00502002
CURRENT FILING DATE: 2001-04-30
PRICR PILING DATE: 2000-12-07
PRICR PLICATION NUMBER: US 09/733,604
PRICR PLICATION NUMBER: US 09/733,604
PRICR PLICATION NUMBER: US 09/736,083
PRICR PLICATION NUMBER: US 05/736,083
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; OTHER INFORMATION: finger
US-09-846-033B-67
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US-09-846-033B-67
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US-09-846-033B-56

Sequence 56, Application US/09846033B

Publication No. US20030044404AI

GENERAL INFORMATION:
APPLICAMT: Rebar, Edward
APPLICAMT: Liu, Oiang
APPLICAMT: Liu, Dei-Qi
APPLICAMT: Wolfe, Alan
APPLICAMT: Wolfe, Alan
APPLICAMT: Sangamo BioSciences, Inc.
APPLICAMT: Sangamo BioSciences, Inc.
APPLICAMT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
TITLE REFERENCE: 019496-00582008
CURRENT APPLICATION NUMBER: US/09/733,604
PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR APPLICATION NUMBER: US 09/736,083

PRIOR PILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 09/736,083

SEQ ID NOS: 252

SOFTWARE: FRASLED for Windows Version 3.0

LENGTH 10 NO 56

LENGTH 1
APPLICANT: Wolffe, Alan
APPLICANT: Estamberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Jarvis, Eric
APPLICANT: Sangame BioSciences, Inc.
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-005820US
CURRENT APPLICATION NUMBER: US/09/846,033B
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 252
NUMBER OF SEQ ID NOS: 252
LENGTH: 7
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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WESULT 14
US-09-846-033B-59
Sequence 59, Application US/09846033B
Sequence 59, Application US/0984603B
Publication No. US20030044404Al
GENEFAL INFORMATION:
APPLICAMT: Rebar, Edward
APPLICAMT: Liu, Pei-Qi
APPLICAMT: Liu, Pei-Qi
APPLICAMT: Wolffe, Alan
APPLICAMT: Sangamo BioSciences, Inc.
APPLICAMT: Sangamo 
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100.0%; Pred. No. 4e+05;
cive 0; Mismatches 0
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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0; Gaps 0; Ouery Match 100.0%; Score 35; DB 9; Length 7; Best Local Similarity 100.0%; Pred. No. 4e+05; Matches 7; Conservative 0; Mismatches 0; Indels

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Search completed: July 15, 2003, 12:57:03 Job time: 17.3333 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 12:53:06 ; Search time 16.3333 Seconds (without alignments)

Perfect score: 36
Perfect score: 36
Sequence: 1 RSDHLSR 7
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:

Published_Applications_AA:*

Database :

/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

# SUMMARIES

Description	Sequence 64, Appl	68,	91,	Sequence 101, App	Sequence 102, App	Sequence 103, App	_	Sequence 105, App	Sequence 106, App	_	111,	Sequence 113, App	Sequence 114, App	Sequence 116, App	Sequence 154, App	Sequence 163, App	Sequence 169, App	Sequence 172, App	Sequence 174, App
ΩI	US-10-006-069A-64	US-10-006-069A-68	US-10-006-069A-91	US-10-006-069A-101	US-10:006-069A-102	US-10-006-069A-103	US-10-006-069A-104	US-10-006-069A-105	US-10-006-069A-106	US-10-006-069A-109	US-10-006-069A-111	US-10-006-069A-113	US-10-006-069A-114	US-10-006-069A-116	US-10-006-069A-154	US-10-006-069A-163	US-10-006-069A-169	US-10-006-069A-172	US-10-006-069A-174
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0; Gaps

100.0%; Score 36; DB 9; Length 7; ilarity 100.0%; Pred. No. 4e+05; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 7; Conserv RSDHLSR 7

1 RSDHLSR 7

QY Dp

Sequence 177, App Sequence 200, App Sequence 64, Appl Sequence 91, Appl Sequence 101, App Sequence 102, App Sequence 103, App Sequence 106, App Sequence 111, App Sequence 111, App Sequence 114, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 117, App Sequence 163, App Sequence 163, App Sequence 177, App Sequence 200, App Sequence 200, App Sequence 200, App Sequence 200, App Sequence 217, App Sequence 200, App Sequence 200, App Sequence 229, App Sequence 229	h Zinc
US-10-006-069A-177 US-10-006-069A-200 US-09-846-033B-64 US-09-846-033B-101 US-09-846-033B-102 US-09-846-033B-102 US-09-846-033B-103 US-09-846-033B-103 US-09-846-033B-105 US-09-846-033B-1105 US-09-846-033B-111 US-09-846-033B-113 US-09-846-033B-115 US-09-846-033B-116 US-09-846-033B-116 US-09-846-033B-116 US-09-846-033B-116 US-09-846-033B-169 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177 US-09-846-033B-177	ALIGNMENTS  69.A-64  64, Application US/10006069A  ion No. USZ0030021776al  INFORMATION:  TO Jamieson, Andrew NT: Liu, Pel-01  NT: Liu, Oldrey, Stephen P.  NT: Liu, Pel-01  NT: Liu, Oldrey, Stephen P.  NT: Application of Angiogenesis With  NT: Sangamo BioSciences, Inc.  NT: Liu, Oldrey, Stephen P.  PELION NUMBER: US/09/73,083  FILING DATE: 2000-12-17  PPLICATION NUMBER: US 09/736,083  ILING DATE: 2000-12-12  PPLICATION NUMBER: US 09/736,083  ILING DATE: 2001-12-12  PPLICATION NUMBER: US 09/736,083  ILING DATE: 2001-12-12  PPLICATION NUMBER: US 09/736,083  ILING DATE: 2001-14-30  DF SEQ ID NOS: 25-2  E: FastSEQ for Windows Version 3.0  O 64  NT: Thing DATE: NUMBER: US 09/846,033  ILING DATE: 2001-12-12  PRI THING DATE: 2001-12-12  PRI T
<i></i>	ALI  -069A-64  ce 64, Application US/10006069A  tition No. US20030021776A1  ANT: Rebar, Edward  ANT: Jamieson, Andrew  ANT: Liu, Qiang  ANT: Liu, Qiang  ANT: Liu, Qiang  ANT: Elsenberg, Eric  ANT: Jarvis, Eric  ANT: Jarvis, Eric  ANT: Sangamo BioSciences, Inc  OF INVENTION: Regulation of An  OF INVENTION: Regulation of An  OF INVENTION: Funger Proteins  REFERENCE: 019496-005830US  TO THING DATE: 2000-12-07  APPLICATION NUMBER: US 09/736,  FILING DATE: 2000-12-12  APPLICATION NUMBER: US 09/736,  FILING DATE: 2000-12-12  APPLICATION NUMBER: US 09/736,  FILING DATE: 2001-12-07  APPLICATION NUMBER: US 09/736,  FILING DATE: 2001-04-30  OF SEQ ID NOS: 252  NEE: FastSEQ for Windows Version  NO 64  H: 7  PRT  INSM: Artificial Sequence  INSPENDATION: finger  INFORMATION: finger
<b>୦ ୦ ୦ ୦ ୦ ୦ ୦ ୦ ୦ ୦ ୦ ୦ ୦ ୦ ୦ ୦ ୦ ୦ ୦ </b>	SULT 1 Sequence 64, Applicat Sequence 64, Applicat Publication No. US200 GENERAL INFORMATION: APPLICANT: Jamleson APPLICANT: Liu, Pei APPLICANT: Liu, Pei APPLICANT: Elsenber APPLICANT: Elsenber APPLICANT: Elsenber APPLICANT: Elsenber APPLICANT: Elsenber APPLICANT: Bangamo TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 0194 CURRENT APPLICATION NU PRIOR FILING DATE: 2 PRIOR APPLICATION NU PRIOR FILING DATE: 2 PRIOR FILING DATE: 3 PRIOR FILING DATE: 3 PRIOR FILING DATE: 2 PRIOR FILING DATE: 3 PRIOR FIL
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APPLICANT Jamieson, Andrew
APPLICANT Liu, Qiang
APPLICANT: Liu, Olang
APPLICANT: Liu, Pel-Oi
APPLICANT: Liu, Pel-Oi
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Sangamo BioSciences, Inc.
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
GURRENT APPLICATION NUMBER: US/10/006,069A
CURRENT APPLICATION NUMBER: US/10/006,069A
PRIOR FILING DATE: 2000-12-17
                                                                                                                       Length 7;
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                                                                                                                ; Score 36; DB 9;
; Pred. No. 4e+05;
0; Mismatches 0
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 101
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PRIOR FILING DATE: 2000.12-12
PRIOR APPLICATION NUMBER: US 09/846,033
PRIOR FILING DATE: 2001-04-30
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GENERAL INFORMATION:
APPLICANT: Bear, Edward
APPLICANT: Jiu, Olang
APPLICANT: Liu, Pet-Qi
APPLICANT: Hu, Pet-Qi
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Arvis, Elsenberg, Stephen P.
APPLICANT: Sangamo BioSciences, In
                                                                                                                  100.0%;
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                        ; FEATURE:
; OTHER INFORMATION: finger
US-10-006-069A-91
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US-10-006-069A-102
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APPLICANT: Jarvis, Eric
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-005830US
CURRENT APPLICATION NUMBER: US/10/006,069A
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-07
PRIOR PELING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-13
PRIOR FILING DATE: 2000-12-13
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Eisenberg, Stephen P.
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Feiglation of Angiogenesis With Zinc
TITLE OF INVENTION: Feiglation of Angiogenesis With Zinc
TITLE OF INVENTION: Feiglation of Angiogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-005830US
CURRENT APPLICATION NUMBER: US/10/006,069A
CURRENT FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR PLING DATE: 2000-12-12
PRIOR PLING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
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Pred. No. 4e+05;
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SOFTWARE: FastSEQ for Windows Version 3.0
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US-10-006-069A-91
; Sequence 91, Application US/10006069A
; Publication No. US20030021776A1
; GENERAL INFORMATION:
                                                                Sequence 68, Application US/10006069A Publication Wo. US20030021776A1 GENERAL INFORMATION:
APPLICANT: Rebar, Edward
                                                                                                                                                                                                                                                              Eisenberg, Stephen P.
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                            Jamieson, Andrew
Liu, Qiang
Liu, Pei-Qi
Wolffe, Alan
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Best Local Similarity 100.
Matches 7; Conservative
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                                          US-10-006-069A-68
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APPLICANT:
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; OTHER INFORMATION: finger US-10-006-069A-105
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Sequence 103, Application US/10006069A

GENERAL INFORMATION:
APPLICANT: Edward
APPLICANT: Liu, Qiang
APPLICANT: Seagementy, Stephen P.
APPLICANT: Sangamen BioSciences, Inc.
APPLICANT: Sangamen BioSciences, Inc.
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc;
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc;
TITLE OF INVENTION: Ringer Proteins
FILE REFERENCE: 019466-005830US
CURRENT APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-17
PRIOR PPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-13-12
PRIOR FILING DATE: 2000-13-13
PRIOR FILI
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100.0%; Pred. No. 4e+05;
tive 0; Mismatches 0
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Pred. No. 4e+05;
; Mismatches 0
           CUKKENT FILING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: US 09/733,604

PRIOR FILING DATE: 2000-12-07

PRIOR FILING DATE: 2000-12-12

PRIOR FILING DATE: 2000-12-12

PRIOR FILING DATE: 2000-12-12

PRIOR FILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 252

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 102
CURRENT APPLICATION NUMBER: US/10/006,069#
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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Gaps
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GENERAL INVENTALION:
GENERAL INVENTALION:
GENERAL INCRANTINE
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APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Holfe, Alan
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Sangamo BioSciences, Inc.
FILE REFERENCE: 019496-005830GS
CURRENT APPLICATION NUMBER: US 09/735,083
PRIOR FILING DATE: 2000-12-12
SEQ. ID NOS: 252
SOFTWARE: FastSEQ for Windows Version 3.0
INUMBER OF SEQ ID NOS: 252
INUMBER OF SEQ ID NOS: 252
INUMBER OF SEQ ID NO 104
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APPLICANT: Liu, Pei-Qi
APPLICANT: Liu, Pei-Qi
APPLICANT: Liu, Pei-Qi
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
TITLE OF INVENTION: Finger Proteins
TITLE OF INVENTION: Pinger 105/10/006,069A
CURRENT FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR PEILNG DATE: 2000-12-12
PRIOR PILING DATE: 2000-12-12
PRIOR PILING DATE: 2000-14-30
PRIOR FILING DATE: 2001-04-30
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Pred. No. 4e+05;
Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 105
LENGTH: 7
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Best Local Similarity 100.0%;
Matches 7; Conservative 0
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ORGANISM: Artificial Sequence
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APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
CTHER INFORMATION: finger
US-10-006-069A-104
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US-10-006-069A-105
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APPLICANT: L14, Pel-Q1
APPLICANT: L14, Pel-Q1
APPLICANT: L14, Pel-Q1
APPLICANT: L14, Pel-Q1
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Estenberg, Stephen P.
APPLICANT: Bangamo BloSciences, Inc.
APPLICANT: Sangamo BloSciences, Inc.
APPLICANT: Jarvis, Eic
APPLICANT: Jarvis, Eic
APPLICANT: Jarvis, Eic
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc
TITLE OF INVENTION: Elnger Proteins
FILE REFERENCE: 014446-005830US
CURRENT APPLICATION NUMBER: US 09/733,604
PRIOR PILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR APPLICATION NUMBER: US 09/846,033
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 111
                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 36; DB 9; Length 7; Best Local Similarity 100.0%; Pred. No. 4e+05; Matches 7; Conservative 0; Mismatches 0; Indels
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                        PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 09/846,033
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 109
LENGTH: 7
  PRIOR APPLICATION NUMBER: US 09/736,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 111, Application US/10006069A Publication No. US20030021776A1 GENERAL INFORMATION: APPLICANT: Rebar, Edward APPLICANT: Jamieson, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 113, Application US/10006069A Publication No. US20030021776Al GENERAL INFORMATION: APPLICANT: Rebar, Edward APPLICANT: Jamieson, Andrew
                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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Matches 7; Conservative
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US-10-006-069A-113
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APPLICANT: Rebar, Edward
APPLICANT: Liu, Otang
APPLICANT: Liu, Pet-Q1
APPLICANT: Liu, Pet-Q1
APPLICANT: Liu, Pet-Q1
APPLICANT: Wolffe, Alar
APPLICANT: Sangamo Blosciences, Inc.
APPLICANT: Jarvis, Eric
APPLICANT: Jarvis, Eric
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
TITLE OF INVENTION: Regulation of Angiogenesis
FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: RestSEQ for Windows Version 3.0
SEQ ID NO 106
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APPLICANT: Liu, Pei-Ol
APPLICANT: Liu, Pei-Ol
APPLICANT: Wolffe, Alan
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Sangamo BloSciences, Inc.
APPLICANT: Sangamo BloSciences, Inc.
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REPRENCE: 019496-0058300S
CURRENT APPLICATION NUMBER: US/10/006,069A
                        100.0%; Score 36; DB 9; Length 7; 100.0%; Pred. No. 4e+05;
                                                                             0; Indels
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Publication No. US20030021776A1
GENERAL INFORMATION:
APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.0
Query Match
Best Local Similarity 100.
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Gaps

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APPLICANT: Janueson, Andrew
APPLICANT: Liu, Pei-Oi
APPLICANT: Liu, Pei-Oi
APPLICANT: Liu, Pei-Oi
APPLICANT: Wolffe, Alon
APPLICANT: Sisonberg, Stephen P.
APPLICANT: Sangamo BioSciences, Inc.
APPLICANT: Sangamo BioSciences, Inc.
APPLICANT: Penger Proteins
TITLE OF INVENTION: Finger Proteins
FILE OF INVENTION: Finger Proteins
FILE OF INVENTION: Finger Proteins
FILE OF INVENTION: Poly 6-005830US
CURRENT APPLICATION NUMBER: US/10/006,069A
CURRENT FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Jarvis, Eric
APPLICANT: Sangame BioSciences, Inc.
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REPREBUCE: 019496-005830US
CURRENT PAPLICATION NUMBER: US/10/006,069A
CURRENT FILING DATE: 2001-12-17
PRICA APPLICATION NUMBER: US 09/733,604
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                                                                                                                                                                 Sequence 116, Application US/10006069A Publication No. US20030021776A1 GENERAL INFORMATION: APPLICANT: Rebar, Edward APPLICANT: Jamieson, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-12-07
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APPLICANT: Jamlesson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Oi
APPLICANT: Wolffe, Alan
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                                                                                                                       RESULT 14
US-10-006-069A-116
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APPLICANT:
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                                 APPLICANT: Eisenberg, Stephen P.
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Jarvis, Eric
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE OF INVENTION: Pogganus
CURRENT APPLICATION NUMBER: US/17/006,069A
CURRENT FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Qi
APPLICANT: Liu, Pei-Qi
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bangamo BioSciences, Inc.
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFERENCE: 019496-005830US
CURRENT APPLICATION NUMBER: US,10/006,069A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 9; Length 7; Pred. No. 4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2001-04-30
NUMBER: OF SEQ ID NOS: 252
SEQ ID NO 114
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 114, Application US/10006069A
Publication No. US20030021776A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0
Best Local Similarity 100.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: finger US-10-006-069A-113
                       Wolffe, Alan
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0; Gaps

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; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 154
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FARTURE:
; OTHER INFORMATION: finger
US-10-006-069A-154
Query Match
Best Local Similarity 100.0%; Score 36; DB 9; Length 7;
Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLSR 7

Db 1 RSDHLSR 7
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Search completed: July 15, 2003, 12:57:03 Job time: 16.3333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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· protein search, using sw model OM protein July 15, 2003, 12:48:06; Search time 33.3333 Seconds (without alignments) 27.983 Million cell updates/sec Run on:

US-10-006-069A-247 36 1 TSGHLSR 7 Perfect score: Sequence: Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:* A_Geneseq_101002:* Database :

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT;

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1998.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description		Human VEGF-targete	Zinc finger protei	Human VEGF-targete	Human VEGF-targete	Zinc finger protei					
ΙD	i	ABJ03962	ABP48959	ABJ03960	ABJ03963	ABP48380	ABP48797	ABP48798	ABP48802	ABP49078	ABP49085
e G		23	23	23	23	23	23	23	23	23	23
* Query Match Length DB		7	7	7	7	7	7	7	7	7	7
% Query Match		100.0	100.0	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7
Score		36	36	33	33	33	33	33	33	33	33
Result No.		-	7	e	❖	S	9	7	80	6	10

Zinc finger protei Zinc finger protei Zinc finger protei	idopsis	Arabidopsis thalia Arabidopsis thalia	ď	bidopsis	Human protein tyro	Human serine-threo	Novel protein kina	Human serine-threo	VEGF-t	finger	inc finger	inc finger		finger	finger	finger	finger	finger	finger	Zinc finger protei	Propionibacterium	Propionibacterium	Arabidopsis thalia	Pinus radiata cell	S	Ø	S	Arabidopsis thalla	Ø	Ω.	Arabidopsis thalla
ABP49088 ABP49102 ABP48958	AAG14909	4908	AAE02543	AAG45426	0665	9279	5695	AAU79280	13964	8743	ABP48746	ABP48749	8752	8755	ABP48758	ABP48761	ABP48764	ABP49007	ABP49010	ABP49019	AAU46550	AAU67542	AAG23358	AAB25136	AAG23357	AAG23356	AAG22824	AAG51268	AAG51272	AAG22823	1267
ABP4 ABP4 ABP4	AAGI	AAG14	AAEC	AAG4	AAEC	AAU7927	AAB6569	AAU7	ABJ0396	ABP4874	ABP4	ABP4	ABP4875	ABP4875	ABP4	ABP4	ABP4	ABP4	ABP4	ABP4	AAU4	AAU6	AAG2	AAB	AAG	AAG2	AAG2	AAG	AAG	AAG	AAG
2333	57	7.7	22	23	22	23	22	23	23	23	23	23	23	23	53	23	23	23	23	23	22	22	21	21	21	21	21	21	21	21	21
~~~	284	302	302	303	356	542	265	280	7	7	7	7	7	7	7	7	7	7	7	7	25	137	171	173	196	199	229	229	229	254	254
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12	14	10	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ABJ03962 standard; Peptide; 7 AA. ABJ03962; RESULT 1 **ABJ**03962

25-SEP-2002 (first entry)

Human VEGF-targeted zinc finger protein fragment SEQ ID NO: 247 Zinc finger protein; angiogenesis; vasculogenesis; ischaemia;

diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclesotic; vasotropic; antiarthritic; vulnerary; antilocer; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.

Homo sapiens

WO200246412-A2.

13-JUN-2002

06-DEC-2001; 2001WO-US46861.

07-DEC-2000; 2000US-0733604. 12-DEC-2000; 2000US-0736083. 30-APR-2001; 2001US-0846033.

(SANG-) SANGAMO BIOSCIENCES INC.

Eisenberg SP; Jamieson A, Liu Q, Liu P, Wolffe A, Rebar E, Jarvis E;

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finger such that it binds to the S3 target subsite, thus designing (I)
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                                                                                                                                                        The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endochelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention.
                               New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of the gene and for treating atherosclerosis, ischemia, arthritis, wound or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc finger protein; ZFP; DNA binding protein; zinc finger.
                                                                                                                                                                                                                                                                                                                                      Length 7;
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                                                                                                                                                                                                                                                                                                                                100.0%; Score 36; DB 23;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
                                                                                                                        Claim 4; Page 103; 195pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SANG-) SANGAMO BIOSCIENCES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-NOV-2000; 2000US-0716637
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100...
7; Conservative
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WPI; 2002-527918/56
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                                                                                                                                                                                                                                                                                                 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP48959;
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
ABP48959
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that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71211 to ABQ72214 and ABB48191 to ABB51230 represent DNA target sequences and zinc finger peptides which are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antitatherosclerotic; vasotropic; antiarthritic; vulnerary; antiuleer; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 36; DB 23;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABJ03960 standard; Peptide; 7 AA
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12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
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Best Local Similarity 100.v..
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TSGHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TSGHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                            7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200246412-A2.
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30-APR-2001;
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Jarvis E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                            diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary; antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating anglogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischemenia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of the gene and for treating atherosclerosis, ischemia, arthritis, wound or
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                    Human VEGF-targeted zinc finger protein fragment SEQ ID NO: 248.
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                                                                                                                                                                                                                                                                                                                 Zinc finger protein; angiogenesis; vasculogenesis; ischaemia;
                                                  Length 7;
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                                                Score 33; DB 23; Length 7;
Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 23; Length 7;
Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wolffe A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu Q, Liu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 103; 195pp; English.
                                                                                                                                                                                                     ABJ03963 standard; Peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SANG-) SANGAMO BIOSCIENCES INC
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85.7%;
                                                  91.7%;
85.7%;
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12-DEC-2000; 2000US-0736083.
30-APR-2001; 2001US-0846033.
                                                                                                                                                                                                                                                           (first entry)
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shown in the invention.
shown in the invention
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                                     WPI; 2002-527918/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 6; Conserv
                                                                                                         1 TSGHLSR 7
                                                                                                                        7 AA;
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Jarvis E;
                         Sequence
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) zinc finger, ordered FY, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (SI), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polypuclectide (III) encoding (I) or (III); and (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsite. (I) is useful for sucception of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I) (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (1) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ7214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                Zinc finger protein related peptide motif SEQ ID NO:393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in the exemplification of the present invention.
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                                          ABP48380 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2001; 2001WO-US43438.
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                                                                                                                          28-AUG-2002 (first entry)
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-500284/53.
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                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu Q;
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1 TSGHLTR 7

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1 TSGHLSR 7 TSGHLAR 7

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RESULT 6 ABP48797

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Zinc finger protein; ZFP; DNA binding protein; zinc finger.
                                       Zinc finger protein related peptide motif SEQ ID NO:738.
              28-AUG-2002 (first entry)
                                                                                                                            WO200242459-A2.
                                                                                       Homo sapiens.
Synthetic.
                                                                                                                                                     30-MAY-2002
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ID ABP4
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AC ABP4
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DT 28-A
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                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) zinc finger, ordered FI, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (CI) comprising (I); (2) a polynuclectide (III) encoding (I) or (II); and (S3) designing (I); (2) a polynuclectide (III) encoding (I) or (III); and (S3) designing (I); (I) involves selecting the F2 zinc finger such that (I) binds to the S1 target subsite, and selecting the F3 zinc (I binds to the S2 target subsite, and selecting the F3 zinc (I binds to that it binds to the S3 target subsite, thus designing (I) chat binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsites and plant engineering (I), (II) or (III) is useful in the subsite specific detection of the rapeutics and plant engineering (I), (II) or (III) is useful in the specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity conditions of the present blanch are given the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                     New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                 Zinc finger protein; ZFP; DNA binding protein; zinc finger
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Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                          2inc finger protein related peptide motif SEQ ID NO:1147.
                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 42; 81pp; English.
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 ABP48797 standard; Peptide; 7 AA
                                                                                                                                                                                                                                                                SANG-) SANGAMO BIOSCIENCES INC
                                                                                                                                                                                                                                       20-NOV-2000; 2000US-0716637.
                                                                                                                                                                                                                20-NOV-2001; 2001WO-US43438
                                                  (first entry)
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                               WPI; 2002-500284/53.
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                                                                                                                                                             WO200242459-A2.
                                                                                                                            Homo sapiens.
                                                  28-AUG-2002
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                                                                                                                                        Synthetic
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ID ABP4
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AC ABP4
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) a target site, comprising a first (FI), a second (F2), and a third (F3) tranger, ordered FI, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (III); and (I) involves selecting the F1 zinc finger such that the binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that it binds to the S3 target subsite, thus designing (I) that binds to a target subsite. (I) is useful for recognition of the carget subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in the such of sequence specific detection of the carget nucleic and plant engineering (I), (II) or (III) is useful in the analyset, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity the contraction of the subsite of modulate the expression of a target region within the subsite of the subsi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 42; 81pp; English.
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                                                                                                                                                                                                                                                      (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                    20-NOV-2000; 2000US-0716637.
20-NOV-2001; 2001WO-US43438
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Best Local Similarity 85.7
Matches 6; Conservative
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WO200242459-A2. Homo sapiens. Synthetic.

30-MAY-2002.

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The present in whention describes a zinc inger protein (1) that binds to zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site, comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (1); (2) a polynucleotide (III) encoding (1) or (II); and (3) target subsite. Also described are: (1) a polypeptide (II) comprising (M) (I) involves selecting the F2 zinc finger such that the binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc that the binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of the target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutics and function of modulate the expression of a target region within the subject, in diagnostic methods for sequences specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity on specificity for their target sequences, as well as enhanced biological activity. ABG71213 and ABB48191 to ABB51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a zinc finger protein (I) that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                        New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
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                                       Zinc finger protein; ZFP; DNA binding protein; zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%; Score 33; DB 23; Length 7; 85.7%; Pred. No. 7.8e+05; ive 1; Mismatches 0; Indels
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Zinc finger protein related peptide motif SEQ ID NO:944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 42; 81pp; English.
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                                                                                                                                                                                                                                                                                                                    (SANG-) SANGAMO BIOSCIENCES INC
                                                                                                                                                                                                                                 20-NOV-2001; 2001WO-US43438
                                                                                                                                                                                                                                                                          20-NOV-2000; 2000US-0716637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-500284/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TSGHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||||:|
1 TSGHLTR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA;
                                                                                                                                              WO200242459-A2.
                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
                                                                                                                                                                                       30-MAY-2002
                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                             Liu 0;
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Matches
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) is a target site, comprising a first (FI), a second (F2), and a third (F3) target site comprises, in 3'-5' direction, a first (SI), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polypucieotide (III) encoding (I) or (III); and (II) involves selecting the F1 zinc finger such that the binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering (I), (II) or (III) is useful in therapeutics specific detection of a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity and specificative for their target sequences, as well as enhanced biological activity. AB071213 to AB071214 and AB048191 to AB051230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                             New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 23; Length 7; Pred. No. 7.8e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 45; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP49085 standard; Peptide; 7 AA.
                                                                                                                                                                                                                      (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.7%;
85.7%;
                                                                                                                                                                                  20-NOV-2000; 2000US-0716637.
                                                                                                                                             20-NOV-2001; 2001WO-US43438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                WFI; 2002-500284/53.
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                         C-terminus
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Synthetic.
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                                                                                                                                                                                                                                                           Liu 0;
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ABP49085
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) at target site, comprising a first (FI), a second (F2), and a third (F3) target site comprises, in 3'-5' direction, a first (SI), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (CI) comprising (I); (2) a polynuclectide (III) encoding (I) or (III); and (S3) target subsite. Also described are: (I) a polypeptide (CI) comprising (I); (2) a polynuclecting the F1 zinc finger such that the binds to the S1 target subsite, and selecting the F2 zinc finger such that it binds to the S3 target subsite, in thus designing (I) that binds to a target site. (I) is useful for recognition of the companient of the binds to a target site. (I) is useful in the 5'-most position of the therapeutics and plant engineering (I). (II) or (III) is useful in therapeutics and plant engineering (I). (II) or (III) is useful in the sample, and in assays to determined the charget nucled acid in a sample, and in assays to determined the charget and specificity for their target sequences, as well as enhanced bloogloal activity. ABG71213 to ABG71214 and ABP48191 to ABP51230 crepresent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                 New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%; Score 33; DB 23; Length 7; 85.7%; Pred. No. 7.8e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zinc finger protein related peptide motif SEQ ID NO:1044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 45; 81pp; English.
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                                                                                                                                                                             (SANG-) SANGAMO BIOSCIENCES INC
                                                          20-NOV-2001; 2001WO-US43438.
                                                                                                               20-NOV-2000; 2000US-0716637
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                            WPI; 2002-500284/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA;
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30-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-terminus
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                                                                                                                                                                                                                                    Liu 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus; where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) encoding (I) or (II); and (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that the binds to the S2 target subsite, and selecting the F3 zinc finger such that the binds to the S3 target subsite, and selecting the F3 zinc finger such that binds to a target site. (I) is useful for recognition of triplet that binds to a target site. (I) is useful for recognition of the causaite. (I) is useful in studying gene function, and for human it can be subsite. (I) is useful in studying gene function, and for human is a subject. In diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the compensation of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced contropred and function of gene expression. (I) has improved affinity and specificative for their target sequences, as well as enhanced contropred the process and zinc finger peptides which are given the become in the sequence in the procession of the procession of the procession in the procession of the procession DNA target sequences and zinc finger peptides which are given the procession of the procession that the sequence is an enhanced and procession of the procession that the sequences and zinc finger peptides which are given the procession of the procession that the sequences and zinc finger peptides which are given the sequences.
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                                                                                                                                                                                                                                                             (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                           20-NOV-2001; 2001WO-US43438
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les 6; Conser
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1 TSGHLTR 7
                        WO200242459-A2.
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Sequence

Query Match

Best Loc Matches

ò 윤 Synthetic.

ABP49088;

RESULT 11 ABP49088

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Gaps

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25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
                                                                                                              C-terminus
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AAG14909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (SI), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polynuclectide (III) encoding (I) or (III); and (I) involves selecting the F1 zinc finger such that the binds to the S1 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that binds to the S1 target subsite, and selecting of F1 zinc finger such that binds to the S1 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human thermal such distribute the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the blenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. AB071213 to AB072214 and AB048191 to AB051230 in the exemplification of the present invention.
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                                                                                                         New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 7;
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Pred. No. 7.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc finger protein related peptide motif SEQ ID NO:996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               in the exemplification of the present invention.
                                                                                                                                                                       Example 1; Page 45; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP48958 standard; Peptide; 7 AA.
                                    (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91:78;
85.78;
           20-NOV-2000; 2000US-0716637.
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                                                                                   WPI; 2002-500284/53
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 AA;
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Synthetic.
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ABP48958
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) care tringer, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) encoding (I) or (II); and (I) (I) a polynuclectide (III) encoding (I) or (III); and (I) (I) involves selecting the F1 zinc finger such that the binds to the S1 target subsite, and selecting the F3 zinc (Inger such that it binds to the S2 target subsite, and selecting the F3 zinc that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsites having the nucleotide G in the 5'-most position of the subsite (I) is useful in studying gene function, and for human thermody to modulate the expression of a target region within the a subsite; and plant engineering (I), (II) or (III) is useful in the anotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced belongical activity. ABG71211 and ABB48191 to ABP51330 crepresent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.
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                                                                                                                                                                                                         New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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(SANG-) SANGAMO BIOSCIENCES INC.
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1e+02;
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PR 21-UUL-1999; 99US-0153103.

PR 21-
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sp_plant:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fung1:* SPTREMBL_21:* sp_mhc: * Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	087366 staphylococ	Q9c410 candida alb	Q8vib4 mus musculu	Q9m142 arabidopsis	Q8vpm4 micrococcus	Q91wy8 oryza sativ	Q9nwv6 homo sapien	Q96c45 homo sapien	Q9d4h6 mus musculu	046363 crithidia f	Q9d112 mus musculu	Q9jm97 mus musculu	Q9asal oryza sativ	Q91qz9 arabidopsis	017595 caenorhabdi	045110 caenorhabdi	
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17 18 19 19 20 21 22 23 31 31 32 33 34 34 36 36 37 40 41 30 42 30 31 31 32 33 34 36 37 38 39 30 30 30 30 30 30 30 30 30 30		SULT 1 7366 087366 087366;	01-NOV-1998 01-NOV-1998 01-DEC-2001 Hypothetical Staphylococc				Query Match Best Local Similarity Matches 6; Conserv	1 TSGHLSR : 38 TAGHLSR
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155 AA; 17998 MW; 30AFE0E1BE045D42 CRC64;
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  SEQUENCE
                                                                                                                                                Q9M142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBVPM4;
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                                                                                                                            RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                  Murad A.M.A., Leng P., Straffon M., Wishart J., Macaskill S., Maccallum D., Schnell N., Talibi D., Marechal D., Tekaia F., d'Enfert C., Gaillardin C., Odds F.C., Brown A.J.P.; "NRGI represses yeast-hypha morphogenesis and hypha-specific gene expression in Candida albicans."; EMBO J. 201472-4752(2001).
EMBL; AF321521; AAK09356.1; --
HSSP; P07248; IARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                                                              91.7%; Score 33; DB 3; Length 310; 85.7%; Pred. No. 29; 1.1ve 1; Mismatches 0; Indels
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"New dystrophin-like protein in heart.";
"New dystrophin-like protein in heart.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB063290; BAB79447.1;
-InterPro; IPR000433; Znf_ZZ.
Ffam: PF00569; Zz. 1
SWART; SW00291; ZnF_ZZ; 1
SWART; SR00291; ZnF_ZZ. 1
PROSITE; PS01357; ZF_ZZ_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-HEART;
TakeuchI T.;
"Mouse dystrophin-like gene.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                          1E108C0998A51284 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Dystrophin-like protein (Fragment).
                                 Last sequence update)
Last annotation update)
 310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 AA
                                                                                                                                                                                                                                                         InterPro; IPR000822; Znf_C2H2.
Pfam: PF00096; zf-C2H3; Z.
ProDom: PD000003; Znf_C2H2; 1.
SMART: SM00355; ZnF_C2H2; 2.
PROSITE: PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE: PS50157; ZINC_FINGER_C2H2_1; Z.
PROSITE: PS50157; ZINC_FINGER_C3H2_2; Z.
DNN-binding: Mctal-binding; Zinc-finger.
SEQUENCE 310 AA; 34301 MW; IE108C0998A5
                       Created)
PRT;
                                                                                                                                                          MEDLINE-21423454; PubMed-11532938;
                     01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 85./v.,
6; Conservative
                                                                          Candida albicans (Yeast).
 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                        11111:1
239 TSGHLAR 245
                                                                                                                                                                                                                                                                                                                                                                                                           1 TSGHLSR 7
                                                                                                                                   SEQUENCE FROM N.A. STRAIN-ATCC10261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                               NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LISSUE-HEART;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhong Z., Caspl R., Mincer T., Helinski D., Knauf V., Boardman K., Wilkinson J.E., Shea T., DeLoughery C., Toukdarlan A.;
"A 50 kb plasmid rich in mobile gene sequences isolated from a marine
                                                Gaps
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Plasmid pSD10.
Bacteria: Firmicutes; Actinobacteria: Actinomycetales; Micrococcineae; Micrococcaceae; Micrococcus.
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  Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K., Mayer K.F.X.;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00395; ŜANT; 1.
PROSITE; PS50090; MTB.
DNA-binding; Nuclear protein.
SEQUENCE 285 AA; 31930 MW; 0666490377D0D700 CRC64;
                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created).
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative myb-related DNA-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative glycine_rich cell wall protein.
                                                Η
Score 32; DB 11;
Pred. No. 24;
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88.9%; Score 32; DB 10;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                       285 AA
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                                                0; Mismatches
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Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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FISSUE-LYMPH;
  SEQUENCE
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Q96C45
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-01-001 (TrEMBLrel. 17, Last annotation update)
Similar to Arabidopsis thaliana DNA chromosome 4.
Oryza sativa (Rice)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldese; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao, M., Ohnori Y., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human CDNA sequencing project.";
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                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0644B06.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 368;
                                                           DB 2; Length 305;
                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AP001129; BAA90626.1; -
InterPro: IPR000620; DUF6.
Pfam: PF00892: DUF6; JUF6
SEQUENCE 368 AA; 40102 MW; 056EF1F9059C0470 CRC64;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY034092; AAK62523.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AKOOGS1: BAA91270.1; InterPro; IPR000719; Euk_pkinase.
                                  305 AA; 30088 MW; 8AAD816F9FF392D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0c7-2000 (TrEMBLrel. 15, Created)
01-0c7-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 20, Last annotation update)
CDNA #2002 (TrEMBLrel. 20, Last annotation update)
Homo saplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;9%; Score 32; DB 10;
85;7%; Pred. No. 58;
                                                        Score 32; DB 2
Pred. No. 47;
0; Mismatches
                                                                                                                                                                                       368 AA
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ProDom; PD000001; Euk_pkinase; 2.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                        PRT;
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                                                        88.9%;
                                             Query Match
Best Local Similarity 85.7-
انتم 6; Conservative
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                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Human).
                                                                                                                              184 TGGHLSR 190
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Best Local Similarity
6; Conserve
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19 TSGHLQR 25
                                                                                                       1 TSGHLSR 7
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                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4530;
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                                   SEQUENCE
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Q9LWY8
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Kawai J., Silnagawa A., Fukunishi Y., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Giopori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rieschmann W., Gassterland T., Gissi C., King B., Kochiwa H., Stehli P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Boluga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 65.0 kDa protein.
Hypothetical for whaman).
Endersybta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sukaryota Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090;
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                                                     Length 542,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014794. AAH14794.1;
InterPro; IPR000719; EUk_pkinase.
Probom; PD000001; EUk_pkinase; 2.
Probom; PD000011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Hypothetical protein; Transferase.
SEQUENCE 580 AA; 64973 MW; 61426673F6B2CEAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
542 AA; 60457 MW; 1988711A61EA1AAF CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUNR-2002 (TrEMBLrel. 20, Last annotation update)
4932415A06R1k protein.
                                            DB
85;
                                                                                                                                                                                                                                                                                                                                                                             580 AA.
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                                                                                                              1; Mismatches
                                                  Query Match

88.9%; Score 32;
Best Local Similarity 85.7%; Pred. No.
Matches 6; Conservative 1; Mismatc
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MEDLINE-21085660; PubMed-11217851;
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                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                       1 TSGHLSR 7
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ESR2 OR ERB
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NON_TER
SEQUENCE
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Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Crithidia.
NCBL_TaxID=5656;
                                                                 Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                          88.9%; Score 32; DB 11; Length 910;
85.7%; Pred. No. 1.5e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.1%; Score 31; DB 5; Length 116;
100.0%; Pred. No. 29;
ive 0; Mismatches 0; Indels
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF045246; AAG232813.1;
Interpro; IPR001878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 5.
PRINTS; PR00393; Zf-CZNF; 5.
SRART; SM00343; ZnF_CZHC; 5.
SEQUENCE 116 AA; 12684 MW; F4BD053987585BIA CRC64;
                                                                                                                                                                                                                                     101937 MW; A602520F381A0ECD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           046363;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUNAR-2002 (TrEMBLrel. 20, Last annotation update)
Universal minicircle sequence binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   116 AA
                                                                                                                                                                   Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Euk_pkinase; 2.

SMART; SM00210; S.TKC; 1.

SMART; SM00219; TYFKC; 1.

ATP-binding; Transferase

SEQUENCE 910 AA; 101937 MW; A602520F
                                                                                                                    MGD; MGI:1921622; 4932415A06R1k.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                      Nature 409:685-690(2001).
EMBL; AK016524; BAB30285.1; -.
HSSP; P24941; 1HCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 1110003008R1k protein.
                                                                                                                                                                                                                                                                       Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crithidia fasciculata.
                                                                                                                                                                                                                                                                                                                   111111:
396 TSGHLSQ 402
                                                                                                                                                                                                                                                                                                      1 TSGHLSR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SGHLSR 7
                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Q9D1L2;
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                                                                                                                                                                                                                                                                                                                                                            RESULT 10
046363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
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                                                                                                                                                                                                                          Carraine-C57BL/65: Tissub-Embryo;

X Kawai J., Silnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X Rawai J., Silnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara M., Nishi K., Yoshino H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Saburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Stauki R., Tomita M., Wagner L., Washio T.,

Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullita M., Gariboidi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Rang B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald M., Weltz C., Whittaker C., Williamig L.,

Nordone P., Rang R., Wang K.H., Weitz C., Whittaker C., Williamig L.,

Nordone P., Marchioni L., Washima Y., Kawaji H., Kohtsuki S.,

Nordone P., Sator K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Whittaker C., Williamig L.,

Nordone P., Sator K., Wang K.H., Weitz C., Whittaker C., Williamig L.,

Nordone P., Sator K., Wang K.H., Weitz C., Whittaker C., Williamig L.,

Nordone P., Whittaker C., Williamig L.,

Nordone P., Storch K.-F.,

Nordone P., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Whittaker C., Williamig L.,

Nordone P., Storch K.-F.,

Nordone P., Schoenbach C., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Storch K.-F.,

Nordone P., Schoenbach C., Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BALB/C;
MEDLINE-21311378; PubMed-11418189;
IShibashi O., Kawashima H.;
"Cloning and characterization of the functional promoter of mouse
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Functional annotation of a full-length mouse cDNA collection.";
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Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 AA; 14740 MW; F5B859EECD98D4B8 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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100.0%; Pred. No. 35;
Live 0; Mismatches 0
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Blochim. Blophys. Acta 1519:223-229(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
EMBL; AKO03388; BAB22757.1; -.
MGD; MGI:1923541; 1110003008R1k.
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EMBL; AB034957; BAA92313.1; -.
MGD; MGI:109392; Esr2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.1%;
85.7%;
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Best Local Similarity 85.7°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 AA;
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Best Local Similarity
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                                                                                                                   NCBI_TaxID=10090;
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Gaps

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Length 265;

Score 31; DB 10; Pred. No. 69;

86.1%; 71.4%;

2; Mismatches

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Pfam; PF00098; zf-CCHC; 8.
SMART; SM00343; ZnF_CZHC; 8.
SEQUENCE 265 AA; 29334 MW; BBCD90D691F82762 CRC64;
                                                                                                                                                       Conservative
                                                                                                                             Local Similarity
les 5, Conserv
                                                                                                                                                                                                       1 TSGHLSR 7
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                                                                                                       Query Match
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1017995
1017995
AC 01759
AC 01759
DT 01-JAD
DT
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Matches
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Cheuk R., Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Ioryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0707010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.1%; Score 31; DB 10; Length 153;
85.7%; Pred. No. 39;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002910; BAB40168.1; -. SEQUENCE 153 AA; 17321 MW; 04DADBF74FAB3B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Theologis A., Ecker J.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
EMBL; ACO06434: AAR87117.1;
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                               153 AA
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last anno
                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLE
P0707D10.26 protein.
P0707D10.26.
Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 TSGHLRR 121
                             101 TSGHLS 106
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TSGHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                          09ASA1;
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Matches
                                                                                                                             RESULT 13
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 286;
                                                                                                                                                                                                                                                                                                                                                                                            Ainscough R.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0A28C9170478D85F CRC64;
                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.1%; Score 31; DB 5;
100.0%; Pred. No. 74;
ive 0; Mismatches
                                                                                                                  286 AA
                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: July 15, 2003, 12:54:51
Job time : 25.6667 secs
                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    investigating biology.", Science 282:2012-2018(1998).
EMBL: 281039; CAB02773.1; -.
InterPro; IPR000535; MSP_domain.
Pfam; PP00639; MSP_domain.)
PRINTS; PR01608; BACINYASINC.
SEQUENCE 286 AA, 30470 MW; 0A28
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                 017595,
01-78n-1998 (TrEMBLrel. 05, Cr
01-JAN-1998 (TrEMBLrel. 05, Lk
01-JUN-2002 (TrEMBLrel. 21, Lk
C25D7.2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                           C25D7.2.
Caenorhabditis elegans.
||||::|
172 TSGHIAR 178
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Matches 6; Conserv
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55 SGHLSR 60
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 15, 2003, 12:51:16; Search time 10.6667 Seconds (without alignments) 19:309 Million cell updates/sec Run on:

US-10-006-069A-247 36 1 TSGHLSR 7

Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 segs, 29422922 residues

Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

/cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 104, App	Sequence 13, Appl	14,	2,	'n	12,	18,	Sequence 4, Appli	4	4	4	4	24,	3190	Sequence 11, Appl	11,	7, 4	4,	4	Sequence 13, Appl		18,	2, A	Sequence 4, Appli	æ	Sequence 4, Appli	Sequence 4, Appli
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ID	US-09-228-986-104	US-08-836-620A-13	US-08-836-620A-14	US-08-836-620A-2	US-08-836-620A-5	US-09-173-941-12	US-07-743-518-18	US-08-447-591-4	US-08-450-943-4	US-08-059-031-4	US-08-450-942-4	PCT-US94-05090-4	US-09-069-023-24	US-09-134-001C-3190	US-08-968-563-11	US-08-969-683A-11	US-09-297-928-7	US-08-935-263-4	US-09-594-185-4	US-08-526-136-13	US-08-911-445-18	US-09-182-983-18	US-08-526-136-2	US-08-526-136-4	US-08-971-188-8	US-09-335-409-4	US-09-568-102-4
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Query Match Length DB	173	484	484	485	485	7	40	228	228	228	228	228	272	296	391	391	391	460	460	466	486	486	503	202	631	1832	1832
Query Match	86.1	86.1	86.1	86.1	86.1	83.3	77.8	77.8	77.8	77.8	77.8	77.8	77.8	77.8	•	•	•	77.8	77.8	77.8	٠	•	77.8	77.8		77.8	77.8
Score	31	31	31	31	31	30	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	78
Result No.	1	7	Э	7	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

444	Sequence 4, Appli Sequence 4, Appli Sequence 24, Appl Sequence 50, Appl Sequence 50, Appl	199, 199, 1, 4,	Sequence 5197, Ap Sequence 2, Appl1 Sequence 2, Appl1 Sequence 492, App Sequence 490, App
US-09-567-969-4 US-09-568-480-4 US-09-568-486-4	US-09-568-472-4 US-09-557-899-4 US-08-469-537A-24 US-08-456-647B-50 US-08-237-401A-50	US-08-469-537A-45 US-08-609-049A-19 US-09-170-996-19 US-08-887-534A-14 US-08-361-395-1	US-09-134-001C-5197 US-09-136-073-2 US-09-457-024A-2 US-09-071-035-492 US-09-071-035-490
444	44040	90441	40444
1832 1832 1832	1832 1832 53 54 54	76 171 171 175 244	269 342 342 358 388
77.8 77.8 77.8	77.8 77.8 75.0 75.0	75.0 75.0 75.0 75.0	75.0 75.0 75.0 75.0
78 78 78 78 78	28 27 27 27	722	72 72 72 72
28 29 30	31 33 34 35	36 37 38 39 40	4 4 4 4 4 1 2 2 3 4 4 5 2

ALIGNMENTS

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US-09-228-986-104
US-09-228-986-104
Sequence 104, Application US/09228986
Sequence 104, Application US/09228986
Sequence 104, Application US/09228986
GENERAL INFORMATION:
TITLE OF INVENTION: Use In the Modification of Plant Cells
TITLE OF INVENTION: Compositions is in the Modification of Plant Cell Signalling
TITLE OF INVENTION: USE IN THE WORD APPLICATION NUMBER: US/09/228,986
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PESTSEQ for Windows Version 3.0
SEQ ID NO 104
LENGTH: 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE: GB 9518272.1
FILING DATE: 08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/08836620A; Patent No. 5958710; GENERAL INFORMATION: TITLE OF INVENTION: Orphan receptor COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orphan receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.1
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pinus radiata
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44 TSGHLS 49
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US-08-836-620A-13
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PRIOR APPLICATION DATA:

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Length 485;
                                                                                                                                         TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READBLE FORM:
MEDIUM TYPE: FLORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PatentIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

86.1%; Score 31; DB
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                   PRIOR AND CATELATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE: APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/836,620A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT/EP96/03933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
                                                                 Sequence 2, Application US/08836620A Patent No. 5958710 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08836620A Patent No. 5958710 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
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37 TSGHLS 42
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CORGANISM: Rai
US-08-836-620A-2
                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                         Length 484;
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                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING STSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
                                                                                                                                                                                                                                                                                                                                       DB 2;
69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; DB 2;
Pred. No. 69;
                                                                                                                                                                                                                                                                                                                       86.1%; Scor.
100.0%; Pred. No. v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.1%; Scor.
100.0%; Pred. No. v.,
... 0; Mismatches
APPLICATION NUMBER: 68 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-ARR-1996
PRIOR APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 08-SEP-1995
PRIOR APPLICATION NUMBER: GB 9518272.1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orphan receptor
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08836620A Patent No. 5958710 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-836-620A-13
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Mus musculus US-08-836-620A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.1
Best Local Similarity 100.
Matches 6; Conservative
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NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
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37 TSGHLS 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-836-620A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
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Gaps

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Indels

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Gaps
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; OTHER INFORMATION: codon binding sequence
US-09-173-941-12
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Patent No. 5397696
GENERAL INFORMATION:
APPLICANT: YANAGHARA, RICHARD
APPLICANT: NERDERAR, VIVER R.
APPLICANT: MILLER, MARK
APPLICANT: GARRITO, RALPH M.
TITLE OF INVENTION: PAPUA NEW GUINEA HUMAN T-LYMPHOTROPIC
TITLE OF INVENTION: VIRUS
                                                                                                                                                                                                                                                                                                  Length 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-173-941-12

Sequence 12, Application US/09173941

Fatent No. 6140081

GENERAL MOREMATION:
TITLE OF INVENDATION:
TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
FILE REFERENCE: NOVO081S

CURRENT APPLICATION NUMBER: US/09/173,941

CURRENT FILING DATE: 1998-10-16

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.3%; Score 30; DB 4; Length 7;
85.7%; Pred. No. 1.9e+05;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON
           PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  86.1%; SU
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
FILING DATE: 15-MAR-1996
                                                                                                                                                                   : 485 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                              Query Match 86.1
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 83.3
Best Local Similarity 85.7
Matches 6; Conservative
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37 TSGHLS 42
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                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Mus
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                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                             US-08-836-620A-5
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                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                      TYPE:
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APPLICANT: CARNAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: DECKER, RICHARD H
APPLICANT: DECKER, RICHARD H
APPLICANT: MALLACE, LESLEY
APPLICANT: MIMMS, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTI
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK ROAD
CITY: ABBOTT PARK
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK ROAD
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC Compatible
COMPUTER: IB PC Compatible
COMPUTER: LEAD PC COMPATIBLE
C
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                                                                                                   CUMPUTEK: LDM C. COMPOLIES:
CUMPUTEK: LDM C. COMPOLIES:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,518
FILING DATE: 19910812
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REGISTRATION NUMBER: WIS/5683/84699/SAP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEFAX: 202-861-3000
TELEFAX: 202-861-3000
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SOFTWARE: Patentin Release #1.0, Version #1.25
GURRBWT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,591
FILLIG DATE: 23-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
21;
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: POREMBSKI, PRISCILLA E. REGISTRATION NUMBER: 33,207 REFERENCE/DOCKET NUMBER: 5347.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,031
ELLING DATE: 07-MAY-1993
ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 4, Application US/08447591; Patent No. 5591440; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.8%;
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Best Local Similarity 83.3
Matches 5; Conservative
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
US-07-743-518-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID
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27 TGHLSR 32
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US-08-447-591-4
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708-938-2623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 TSGHLT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-059-031-4
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APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR
TITLE OF INVENTION: DETECTION
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                               Gaps
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                                                                                                                                                                         Length 228;
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                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,943
                                                                                                                                                                         Score 28; DB 1; 1
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 1;
Pred. No. 1.3e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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ep. 5347.US.01
                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08450943
Patent No. 5593825
GENERAL INFORMATION:
APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLIS, LESLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 4:
          INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                       Query Match
Best Local Similarity 83.5.
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Best Local Similarity 83.3
Matches 5; Conservative
708-938-2623
                                                                                                                      ; MOLECULE TYPE: protein US-08-447-591-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                       linear
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                                                                                                       TOPOLOGY:
TELEFAX:
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APPLICANT: MIMMS, LARRY T
APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTI
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLACE, LESLEY
APPLICANT: WALLACE, LESLEY
APPLICANT: MIMMS, LARRY T
APPLICANT: SOLOWON, LARRY R
APPLICANT: ABOLOWON, LARRY R
ADDRESSED: ABBOTT LABORATORIES D377/AP6D
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                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 60064-3500
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/059,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28;
Pred. No. 1
1; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.U
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IE: ABBOTT LABORATORIES ONE ABBOTT PARK ROAD
Sequence 4, Application US/08059031
Patent No. 5595739
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08450942
Patent No. 5925512
                                                                           APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD
APPLICANT: WALLACE, LESLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 77.8
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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us-10-006-069a-247.rai

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GENERAL INFORMATION:

APPLICANT: LYAID DOUGETE-STARM et al
APPLICANT: LYAID DOUGETE-STARM et al
APPLICANT: LYAID DOUGETE-STARM BAINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERHIDES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3190
LENGTH: 296
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GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inchara, Nachiro.
APPLICANT: Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03133
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN VET. 2.0
                                                                                                       Gaps
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                                                               Length 228;
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Pred. No. 1.6e+02;
i; Mismatches 0; Indels
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                                                             Score 28; DB 5;
Pred. No. 1.3e+02;
                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Staphylococcus epidezmidis US-09-134-001C-3190
                                                                                                                                                                                                                                             RESULT 13
US-09-069-023-24
Sequence 24, Application US/09065023A
; Patent No. 6348573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%;
                                                             77.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 77.8
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                       Conservative
MOLECULE TYPE: protein PCT-US94-05090-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
JS-09-069-023-24
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Best Local Similarity
Matches 5; Conserv
                                                             Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                            1 TSGHLS 6
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US-09-134-001C-3190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application PC/TUS9405090
GENERAL INFORMATION:
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLACE, LESLEY
APPLICANT: WALLACE, LESLEY
APPLICANT: WALLACE, LESLEY
APPLICANT: MINKS, LERRY T
APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Pred. No. 1.3e+02;
1; Mismatches 0; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/450,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: ABBOTT LABORATORIES D377/AP6D ONE ABBOTT PARK ROAD
                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELECOMMUNICATION:
TELECHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/ACENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33.207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US94/05090
                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
FRNGTH: 228 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3.
                                                                                                                                                                                                                                                 TELEPHONE: 708-22
TELEPHONE: 708-238-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 708-938-2623 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           708-938-2623
                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                   FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||:
5 TSGHLT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
PCT-US94-05090-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-450-942-4
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Query Match 77.8%; Score 28; DB 3; Length 391; Best Local Similarity 83.3%; Pred. No. 2.3e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: WILMINGFUN
STREE: DELAMARE
COUNTRY: U.S.A.
2IP: 19898
ADDRESSEE: GENENCOR INTERNATIONAL, INC.
STREET: 1870 SOUTH WINTON ROAD
CITY: ROCHESTER
STREET: 1870 SOUTH WINTON ROAD
CITY: ROCHESTER
STRATE: NEW YORK
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: TEMP FOR COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
APPLICATION NUMBER: US/08/968,563
FILING DATE: VOWEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 33,692
FILING DATE: NOWEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: CR-9982
FILING DATE: NOWEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: TOPOLOGY
TOPOLOGY: UNKNOWN
TOPOLOGY: TOPOLOGY
TOPOLOGY: UNKNOWN
TOPOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHOD FOR THE RECOMBINANT
TITLE OF INVENTION: PRODUCTION OF 1,3-PROPANEDIOL
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CARRESPERS: I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                         CHARLES E. NAKAMURA
ANTHONY A. GATENBY
AMY (KUDANG-HUA) HSU
RICHARD D. LA REAU
SHARON L. HAYNIE
MARIA DIAZ-PORRES
DONALD E. TRIMBUR
GREGORY M. WHITED
VASANTHA NAGARAJAN
MARK S. PAYNE
STEPHEN K. PICATAGGIO
RAMESCH V. NAIR
Sequence 11, Application US/08968563
Patent No. 6013494
GENERAL INFORMATION:
APPLICANT: CHARLES E. NAKAMURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein (CRIGINAL SOURCE: ORGANISM: GPD1 US-08-968-563-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: WILMINGTON STATE: DELAWARE
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Job time : 11.6667 secs

Search completed: July 15, 2003, 12:56:10

1 TSGHLS 6

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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein

July 15, 2003, 12:53:06; Search time 16.3333 Seconds (without alignments) 49.894 Million cell updates/sec Run on:

US-10-006-069A-247 36 1 TSGHLSR 7

Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

445758 seqs, 116419773 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length DB	DB	ΙD	Description
	36	100.0	7		TS-10-006-0698-247	and 710 approximate
	90	000	٠ ٢	٠.	1100 000 000 000	ddy / Fr compress
7	30	100.0	`	ע	US-03-846-0338-24/	Sequence 247, App
e	36	100.0	7	σ	US-09-990-186-1201	Sequence 1201, Ap
₹	36	100.0	7	6	US-09-989-994-1201	Sequence 1201, Ap
2	36	100.0	7	10	US-09-989-789-1201	Sequence 1201, Ap
9	33	91.7	7	σ	US-10-006-069A-245	Sequence 245, App
7	33	91.7	7	σ	US-10-006-069A-248	
80	33	91.7	7	6	US-09-846-033B-245	245
6	33	91.7	7	6	US-09-846-033B-248	248
10	33	91.7	7	6	US-09-990-186-393	393,
11	33	91.7	7	6	US-09-990-186-738	
12	33	91.7	7	σ	US-09-990-186-944	944
13	33	91.7	7	σ	US-09-990-186-1036	1036
14	33	91.7	7	6	US-09-990-186-1044	Sequence 1044, Ap
15	33	91.7	7	σ	US-09-990-186-1147	Sequence 1147, Ap
16	33	91.7	7	6	US-09-990-186-1243	Sequence 1243, Ap
17	33	91.7	7	σ	US-09-990-186-1244	1244,
18	33	91.7	7	σ	US-09-989-994-393	
19	33	91.7	7	σ	US-09-989-994-738	

ALIGNMENTS

```
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Jarvis, Eric
APPLICANT: Jarvis, Eric
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
TITLE OF INVENTION: Finger Proteins
FILE REFRENCE: 019446-005830US
CURRENT APPLICATION NUMBER: US/10/006,069A
CURRENT FILING DATE: 2001-12-17
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSEQ for Windows Version 3.0
                     Sequence 247, Application US/10006069A Publication No. US20030021776A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                             GENERAL INFORMATION:
APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Oi
APPLICANT: Molffe, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: finger
US-10-006-069A-247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-006-069A-247
                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Gaps ö 100.0%; Score 36; DB 9; Length 7; 100.0%; Pred. No. 4e+05; Live 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 7; Conservative

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Sequence 1201, Application US/0998994
Publication No. US20030104526A1
GENERAL INFORMATION:
APPLICAMY: LIU, QAENG
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,994
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PATCHIL Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1201, Application US/09989789

Patent No. US20020063379A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SCOTWARE: PATENTIN Ver. 2.0

SEQ ID NO 1201
                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-989-994-1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-989-789-1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 10; Length 7;
Pred. No. 4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 36; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rebar, Edward APPLICANT: Jamieson, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100..
المالية منابعة أنهام 7; Conservative
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Liu, Pei-Qi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TSGHLSR 7
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US-09-989-789-1201
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                                                                                                                                                                                                                                                                                SEQ ID NO 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT
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Publication No. US20030068675A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-990-186-1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                  APPLICANT: Liu, Pei-Qi
APPLICANT: Liu, Pei-Qi
APPLICANT: Liu, Pei-Qi
APPLICANT: Liu, Pei-Qi
APPLICANT: Wolffe, Alan
APPLICANT: Wolffe, Alan
APPLICANT: Sangamo BioSciences, Inc.
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Requilation of Angiogenesis With Zinc
TITLE OF INVENTION: Ringer Proteins
FILE REFERENCE: 019496-0058200US
CURRENT APPLICATION NUMBER: US 09/7346, 033B
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 09/735,004
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 247
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 36; DB 9; Length 7; 100.0%; Pred. No. 4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                         Sequence 247, Application US/09846033B publication No. US20030044404A1 GENERAL INFORMATION:
APPLICANT: Rebar, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                     Jamieson, Andrew
Liu, Qiang
Liu, Pei-Qi
Wolffe, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: finger US-09-846-033B-247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TSGHLSR 7
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                                  US-09-846-033B-247
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Gaps

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RESULT 4

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Gaps

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APPLICANT: Liu, Pei-Oi
APPLICANT: Liu, Pei-Oi
APPLICANT: Liu, Pei-Oi
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Sangamo BioSciences, Inc.
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc
TITLE OF INVENTION: Pringer Proteins
FILE REFERENCE: 01946-0058200S
CURRENT APPLICATION NUMBER: US/09/846,033B
CURRENT FILING DATE: 2000-104-30
PRIOR APPLICATION NUMBER: US 09/735,083
PRIOR PILING DATE: 2000-12-07
PRIOR PILING DATE: 2000-12-07
PRIOR PILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FEASISEQ for Windows Version 3.0
SEQ ID NO 248
                                                                                                                                                              APPLICANT: Liu, Pei-Oi
APPLICANT: Liu, Pei-Oi
APPLICANT: Holffe, Alan
APPLICANT: Holffe, Alan
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bangamo BioSciences, Inc.
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Finger Proteins
TITLE OF INVENTION: Finger Proteins
TITLE OF INVENTION: Finger Proteins
CURRENT APPLICATION NUMBER: US/09/846, 033B
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSED for Windows Version 3.0
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Pred. No. 4e+05;
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                                  Sequence 245, Application US/09846033B Publication No. US20030044404A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 248, Application US/09846033B Publication No. US20030044404A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 85.7%;
Matches 6; Conservative
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                                                                                                                   APPLICANT: Rebar, Edward APPLICANT: Jamieson, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: finger US-09-846-033B-245
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Pred. No. 4e+05;
1; Mismatches 0; Indels
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APPLICANT: Liu, Qiang
APPLICANT: Liu, Pet-Oi
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Javis, Eric
APPLICANT: Sangamo BioSciences, Inc.
TITLE OF INVENTION: Regulation of Anglogenesis With Zinc.
TITLE OF INVENTION: Finger Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 9;
Pred. No. 4e+05;
1; Mismatches
FILE REFERENCE: 019496-005830US
CURRENT APPLICATION WUMBER: US/10/006,069A
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION WUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
PRIOR FILING DATE: 2001-04-30
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 245
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CURRENT APPLICATION NUMBER: US/10/006,069A
CURRENT FILING DATE: 2001-12-17
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 248
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PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-12
PRIOR PLING DATE: 2001-12-13
PRIOR FILING DATE: 2001-04-30
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                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: finger
US-10-006-069A-245
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ORGANISM: Artificial Sequence
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85.7%;
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GENERAL INFORMATION:
APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
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Best Local Similarity 85.73
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS FILE REFERENCE: 8325-0011.21 / S11-US3 CURRENT APPLICATION NUMBER: US/09/990,186 CURRENT FILING DATE: 2001-11-20 NUMBER OF SEQ ID NOS: 4085 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1036, Application US/09990186
Publication No. US20030068675A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOCTWARR: Patentin Ver. 2.0
SEQ ID NO 1036
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Publication No. US20030068675A1
GENERAL INFORMATION:
APPLICANT: LIU, Olang
TITLE OF INVENTION: PROSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERSENCE: 8325-0011.21 / S11-US3
CURRENT FILING DAFE: 2001-11.20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-990-186-944
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Pred. No. 4e+05;
1; Mismatches
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Best Local Similarity 85.7%;
Matches 6; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 85.7
Matches 6; Conservative
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1 TSGHLTR 7
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Publication No. US20030068675A1
GENERAL INFORMATION:
FAPLICANT: LIU, Olang
TITLE OF INVENTION: PROSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SCOTWARR: Patentin Ver. 2.0
SEQ ID NO 393
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Sequence 738, Application US/09990186

Sequence 738, Application US/09990186

GENERAL INFORMATION:

APPLICANT: LIU, 01ang

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.21 / S11-US3

CURRENT FILING DATE: 2001-11-20

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: PATENTIN VET. 2.0
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Pred. No. 4e+05;
    Pred. No. 4e+05;
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Pred. No. 4e+05;
                       1; Mismatches
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  85.78;
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ORGANISM: Artificial Sequence
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Best Local Similarity 85.7-
Best Local Similarity 85.7
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Best Local Similarity 85.7
Matches 6; Conservative
                                                            1 TSGHLSR 7
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US-09-990-186-393
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US-09-990-186-944
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US-09-990-186-1147
; Sequence 1147, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Olang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT APPLICATION NUMBER: US/09/990,186
; SOFTWARE: PATENTING DATE: 2001-11-20
; SOFTWARE: PATENTING OF SEQ ID NOS: 4085
; SOFTWARE: PATENTING OF SEQ ID NOS: 4085
; SOFTWARE: PATENTING OF SEQ ID NO 1147
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; OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-990-186-1044
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Pred. No. 4e+05;
1; Mismatches 0; Indels
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                                                          Length 7;
                                                        Score 33; DB 9;
Pred. No. 4e+05;
1; Mismatches
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ORGANISM: Artificial Sequence
                                                      Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model	July 15, 2003, 16:30:06; Search time 69 Seconds (without alignments) 40.555 Million cell updates/sec
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SEQ55-247-68 107 1 DRSNLTRTSGHLSRRSDHLSR 21 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 segs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description .	HIV-B zinc finger	Drosophila melanog	Propionibacterium	Propionibacterium	Propionibacterium	Asperdillus orvzae	Asperdillus orvzae	5-aminolevulinic a	Human polypeptide	C glutamicum prote
ID	ABB05107	ABB67173	AAU63831	AAU53591	AAU49653	AAW30557	AAW41509	AAW41498	AAM40688	AAG92912
DB	23	22	22	22	22	19	19	19	22	22
% Query Match Length DB ID	21	532	94	89	205.	989	636	636	228	1610
% Query Match	49.5	49.5	45.8	45.3	43.9	43.9	43.9	43.9	43.0	42.1
Score	53	53	49	48.5	47	47	47	47	46	45
Result No.		7	'n	4	S	9	7	80	6	10

Corynebacterium gl Corynebacterium gl B. subtilis rib op Polypeptide encode Zinc finger clone Propionibacterium Propionibacterium Propionibacterium Drosophila melanog Human polypeptide Klebsiella pneumon Drosophila melanog Herbicidally activ Streptococcus poly Zinc finger clone HIV-E zinc finger Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia HIM-E HIM-E ZINGER HIM-E ARABIGOPSIS HABIA	Human polypeptide Human ovarian anti Human cardiovascul Novel ovarian rela Human nervous syst Chlamydia trachoma Streptococcus pneu
22 AAB76516 22 AAB76537 23 AAB76537 24 AAV83269 22 AAV46550 22 AAV46550 22 AAV46550 22 AAV46550 22 AAV46550 22 AAV6655 22 AAV66550 23 ABB6454 20 AAV33371 22 ABB6493 23 ABB62105 23 ABB65105 23 AAB65105 23 AAB65105 23 AAR639667 24 AAG36667 25 AAG36667 26 AAG36667 27 AAG36667 28 AB668897 28 AB668897 21 AAG36665 21 AAG36667 21 AAG36665 22 AAG36667 23 AAG36667 24 AAG36667 25 AAG36667 26 AAG36667 27 AAG36667 28 AAG3667 28 AAG3667	
610 8856 8856 8856 8857 8	1499 2 140 2 140 2 140 2 183 2 250 2 312 1
44444444444444 UUUUUUUUU UUUUUUU UUUUU UUUU UUU UU	
NN NN 4 4 4 4 4 8 8 8 8 8 8 8 8 8 8 8 8	1011111 1444444
11111111111111111111111111111111111111) W 4 4 4 4 4) W 0 H G W 4 W

ALIGNMENTS

RESULT 1
ABB05107
ID AEB05107 standard; Peptide; 21 AA.
XX
AC ABB05107;
XX
DT 27-MAR-2002 (first entry)
XX
Human immunodeficiency virus; HIV; He
XW
Human immunodeficiency virus; HIV; He
XW
M nucleic acid binding protein; viral;
XX
W anti-HIV.
XX
W buman immunodeficiency virus type 1.
XX
W w0200185780-A2.
XX
PD 15-NOV-2001.
XX
PP 08-MAY-2001; 2001WO-GB02017.
XX
PP 08-MAY-2000; 2000GB-0011068.
PR 30-MAY-2000; 2000GB-0013106.
PR 30-MAY-2000; 2000GB-001306.
PR 30-MAY-2000; 2000GB-0013

HIV-B zinc finger amino acid sequence.

Human immunodeficiency virus; HIV; Herpesvirus; HSV; zinc finger; nucleic acid binding protein; viral; promoter; infection; virucide; anti-HIV.

Human immunodeficiency virus type 1. Synthetic.

Choo Y, Demaison C, Moore M, Papworth MA, Reynold L, Ullman CG; Isalan M;

7

seq55-247-68.rag

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genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200181581-A2.
                                                                                                                                          ABB57737-ABB7
              interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                            AAU63831;
                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                                                           AAU63831
  셤
                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                 The present invention describes a polypeptide (I) capable of binding to a nucleic acid comprising a viral nucleotide sequence. Also described a excite; (2) a composition (II) comprising (I) and a exciplent, diluent or carrier; (2) a nucleic acid molecule (III) encoding (I); (3) an expression vector (IV); and (5) modulating transcription by targeting nucleic acid sequences that overlap with transcription factor binding sites by the use of engineered zinc finger molecules. (I) has virucide and conclete and for targeting a native viral nucleic acid molecule, and for targeting a native viral nucleic acid sequence with a nucleic acid binding polypeptide. (I) is also useful for downregulating a viral packagaing or viral transcription in a cell infected with the virus by contacting the virus and/or the cell with (I). (I) is also useful for modulating a viral function in a system. (I) is also useful for modulating a viral function in a system. (I) is nicelules to which they bind. More preferably, they are highly effective in repressing gene expression from the HIV-I promoter. ABBO5064 to event if the present the present sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more
                    Novel viral nucleic acid binding polypeptide useful for binding viral promoter sequences, and modulating expression of gene linked to viral promoter sequence, and for treating human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                        Score 53; DB 23; Length 21;
Pred. No. 0.056;
.; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 28311.
                                                                                                                                                                                                                                                                                                                           exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB67173 standard; Protein; 532 AA.
                                                                              Example 3; Page 73; 141pp; English
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                                                                                                                                                                                                                                                                                                                                                                         49.5%;
83.3%;
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Best Local Similarity 83.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   9 SGHLSRRSDHLS 20
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WPI; 2002-139420/18
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                                                                                                                                                                                                                                                                                                                                                  21 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0156-ABL30511), expressed DNA sequences (ABL01876) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthelmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
SEQ ID NO 28311; 21pp + Sequence Listing; English
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, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID No 25026; 1069pp; English.
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58.8%; Pred. No. 2.3;
11ve 2; Mismatches
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380 RANGTRISSHLGAENDH 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RSNLTRTSGHLSRRSDH 18
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.8
Matches 10; Conservative
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N-PSDB; AAS59636.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 AA;
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pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of p. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention of adtermining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to character treat P. acnes proteins. These antibodies can be used to character treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
             $$$$$$$$$$$$$$$$$$$$$$$$
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94 AA; Sequence

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Gaps
                       5,
  Length 94;
                       Indels
                       2;
 Score 49; DB 22;
Pred. No. 1.5;
          ed. No. 1.5;
Mismatches
                                              20
                                                                    09
Query Match 45.8%;
Best Local Similarity 64.7%;
Matches 11; Conservative
                                              6 TRTSG--HLSRRSDHLS
                                                           |||:| | ||:||||
44 TRTTGHHHQRRRADHLS
                                              ð
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RESULT 4

AAU53591 standard; Protein; 89 AA. AAU53591

AAU53591;

Propionibacterium acnes immunogenic protein #14487. (first entry) 27-FEB-2002

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uvaitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes

WO200181581-A2.

01-NOV-2001.

20-APR-2001; 2001WO-US12865

2000US-199047P. 2000US-208841P. 2000US-216747P. 21-APR-2000; 02-JUN-2000; 07-JUL-2000;

(CORI-) CORIXA CORP.

Wang SS, Mitcham JL, Waus L'maisonneuve J, Zhang'Y, Persing DH, Skeiky YAW,

Bhatia A;

WPI; 2001-616774/71. N-PSDB; AAS59561.

for Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful Example 1; SEQ ID No 14786; 1069pp; English. treating acne vulgaris

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

pustuiosis, imperiosis and observable the pustuiosis, imperiosis and includes to pustuiosis, imperiosis and includes the central nervous system, however it is particularly involved in the inflammatory resisting associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting the sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to therefore treat P. acnes infections. The antibodies may also be used to therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences. pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis

25555555555555555555X&

89 AA; Sequence

Gaps 7; 89; Score 48.5; DB 22; Length Indels 4; Pred. No. 1.7; 3; Mismatches 45.3%; Best Local Similarity 46.2 Matches 12; Conservative Query Match

1;

3 SNLTRTSGHLSR-----RSDHLSR 21 | :| |:|| || || 3 SIVIVITGHISRYYRHGDCRREHLSR

ð g

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RESULT 5

AAU49653 standard; Protein; 205 AA

(first entry) 13-FEB-2002 Propionibacterium acnes immunogenic protein #10549.

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes

WO200181581-A2.

01-NOV-2001.

20-APR-2001; 2001WO-US12865

21-APR-2000; 2000US-199047P. 02-JUN-2000; 2000US-208841P. 07-JUL-2000; 2000US-216747P.

(CORI-) CORIXA CORP.

Bhatia A; Wang SS, ä Mitcham JL, Wany L'maisonneuve J, Zhang Y, DH, Skeiky YAW, Persing

WPI; 2001-616774/71.

N-PSDB; AAS59545

useful for Propionibacterium acnes polypeptides and nucleic acids useful vaccinating against and diagnosing infections, especially usef treating acne vulgaris

SEQ ID No 10848; 1069pp; English. Example 1; Sequences AAU39105-AAU68017 xepresent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

an isolated genomic DNA (see AAV45424).

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ä
                                                                                                                                                                                                        enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Production of polypeptide in respiratory-deficient cells transformed with construct - that complements the defect and encodes polypeptide, also production of defective cells by disrupting gene essential for oxidative phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of 5-aminolevulinic acid synthase (ALAS), an enzyme of the haem biosynthetic pathway, that can be isolated from Aspergillus oryzae strain Al560. The sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5-Aminolevulinic acid synthase; hemA gene; respiratory deficient;
                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                              Length 205;
                                                                                                                                                                                                                                                                                                                                                                2; Indels
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/note= "putative mitochondrial leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus oryzae 5-aminolevulinic acid synthase.
                                                                                                                                                                                                                                                                                                                             Score 47; DB 22;
Pred. No. 7.8;
2; Mismatches 2;
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93 DQHNVTVPQQQRPDNDPRVSGH-SRRSDH 120
                                                                                                                                                                                                                                                                                                                                                                                                1 DRSNLT-----RTSGHLSRRSDH 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW30557 standard; Protein; 636 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jensen EB;
                                                                                                                                                                                                                                                                                                                             ch 43.9%;
1 Similarity 44.8%;
13; Conservative
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                                                                                                                                                                                                                                                                                               205 AA;
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW30557;
                                                                                                                                                                                                                                                                                               Sequence
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method of producing a polypetide comprises: (a) introducing into a respiratory-deficient cell mutant (1) one or more first nucleic acid sequences (NAS) which complement the respiratory defect and (ii) a second NAS which encodes the polypeptide, (b) cultivating the cell in a culture medium under aerobic conditions suitable for expression of the first and second NAS, and (c) isolating the polypeptide from the culture medium. The first NAS encodes a component of the electron transport chain, or an enzyme involved in the biosynthesis of uniquinone, flavino or haem (e.g. ALAS). Also claimed is a respiratory-deficient mutant cell that is haem cellent (see AAV5426). The method is used to select and maintain transformed cells, to ensure high level expression and genetic stability of transformants during culture. It is applicable to all constraint formatical fermentation processes, requiring only that the cells
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5-Aminolevulinic acid synthase; hemA gene; herbicide; haemoprotein.
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                                                                                                                                                                                                                                                                                   DB 19; Length 636;
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/note= "haem regulatory motif"
220..230
/note= "glycine loop involved in pyridoxal
phosphate cofactor binding"
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "mutative mitochrondrial leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus oryzae 5-aminolevulinic acid synthase.
                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "haem regulatory motif"
                                                                                                                                                                                                                                                                                 Score 47; DB 1
Pred. No. 29;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus oryzae strain A1560 (IFO 4177).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..35
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW41509 standard; Protein; 636 AA.
                                                                                                                                                                                                                                                                                                                                                                        549
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                                                                                                                                                                                                                                                                                                                                            1 DRSNLTRTSGHLSRRSDHL 19
                                                                                                                                                                                                                                                                                 43.9%;
                                                                                                                                                                                                                                                                                                                                                                       531 ERLRITPTPGHIKEHRDHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                         need oxygen for growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cherry JR, Elrod SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-052303/05.
N-PSDB; AAV04102.
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                    636 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9747736-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1998
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                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW41509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-aminolevulinic acid synthase; porphobilinogen synthase;
haemoprotein production; filamentous fungus; haeme biosynthetic enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                            synthase) of Aspergillus niger IFO 4177. Its annio acid sequence was deduced from the isolate hemA gene (see AAV04102) and shares 81% identity with the Aspergillus nidulans ALA synthase. The enzyme catalyses the reaction of giycine and succinil-CoA to form 5-aminolaevulinic acid, which is useful as a herbicide. It is also the rate-determining enzyme in biosynthesis of haem in liver cells and differentiating erythrocytes, so overexpression in a cell can be used to increase the yield of haemoproteins produced by the cell in the absence of haemin supplementation. Host cells, especially bacterial, fungal, filamentous fungal and yeast cells, transformed with a vector that includes the hemA gene are claimed, and can be used in a claimed method for producing ALA synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method for the production of haemo:protein in a filamentous fungal cell - by introducing a haeme biosynthetic enzyme coding sequence and control sequences into the cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                   protein comprises the 5-aminolevulinic acid synthase (ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.9%; Scor.
42.1%; Pred. No. 2>,
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Claim 1; Page 26-27; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW41498 standard; Protein; 636 AA
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531 ERLRITPTPGHIKEHRDHL 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-052312/05.
N-PSDB; AAV19709.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          636 AA;
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10-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                      production of the haemoprotein and the haeme biosynthetic enzymes; and (c) recovering the haemoprotein from the nutrient medium of the filamentous fungal cell. The method is used to yield commercially significant quantities of haemoprotein in filamentous fungal strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; .CNS; Alzheimer's; Parkinson's disease; Humtington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
cultivating the filamentous fungal cell in a nutrient medium suitable
                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qian XB,
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tu C, Xue AJ,
Drmanac RT;
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                                                                                                                                                                                                                                    Score 47; DB
Pred. No. 29;
                                                                                                                                                                                                                                                                                                 3; Mismatches
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Wang Z, Wehrman T, Xu C, X
Zhou P, Goodrich E, Drmana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM40688 standard; Protein; 228 AA
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                                                                                                                                                                                                                                                                                                                                                                                                     :| :| || || 549
531 ERLRITPTPGHIKEHRDHL 549
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2000US-052317.
2000US-0598042.
2000US-062012.
2000US-0653450.
2000US-0653450.
2000US-065391.
                                                                                                                                                                                                                                    43.98;
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                                                                                                                                                                                                       Query Match
Best Local Similarity 42...
Best Local Similarity 62...
Account of the construction of the con
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                                                                                                                                                                                636 AA;
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19-OCT-2000;
29-NOV-2000;
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09-JUL-2000;
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Wang J, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM40688;
                                                                                                                                                                                    Sequence
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AAM40688
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Length 1610;

1610 AA;

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Query Match
Best Local Similarity
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               Sequence
                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium and identifying a particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
           utilisation of the activities such as: Immune system suppression, Activity.hibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
Senoh A, Ikeda M, Ozaki A;
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                                                                                                                                                                                                                                                                                                                    Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; SEQ ID NO: 6666; 246pp + Sequence Listing; English.
                                                                                                                                 Score 46; DB 22; Length 228;
Pred. No. 13;
2; Mismatches 2; Indels
                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                            C glutamicum protein fragment SEQ ID NO: 6666.
                                                                                                                                                                                                                                                                    AAG92912 standard; Protein; 1610 AA.
                                                                                                                                   43.0%;
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03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                              :|| :|||| |||
78 SLTASSGHLGRRS 90
                                                                                                                                                                                  4 NLTRISGHLSRRS 16
                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                              organic acid synthesis.
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                                                                                                                                   Query Match
Best Local Similarity
                                                                                                          228 AA;
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Tateishi N,
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                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                        membrane construction and membrane transport protein; petroleum spill; ydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation; genome mapping; genetic engineering.
                                        Gaps
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                                      10; Indels
                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum MCT protein SEQ ID NO:14.
Score 45; DB 22;
Pred. No. 1.8e+02;
2; Mismatches 10,
                                                                                                                                                                                                         AAB76516 standard; Protein; 1610 AA.
                                                                                                               1588 DEPEIGTVGAHLSRRIDEISR 1608
                                                                          1 DRSNLTRTSGHLSRRSDHLSR 21
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99DE-1032124.
99DE-1032125.
 42.18;
ilarity 42.98;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200100805-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-2000;
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                                                                                                                                                                                                                                             AAB76516;
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7-AUG-1
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Bacillus subtilis
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                                                                                                                                          AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.

AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum; brevibacterium lactofermentum; MCT; membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation; genome mapping; genetic engineering.
                                                              Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation -
                                                                                                                                                                                                                                                                                                                   Gaps
         Haberhauer G;
                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                             Length 1610;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum MCT protein SEQ ID NO:56.
                                                                                                                                                                                                                                                                                          Query Match 42:1%; Score 45; DB 22; Le
Best Local Similarity 42:9%; Pred. No. 1.8e+02;
Matches 9; Conservative 2; Mismatches 10;
         Zelder O,
                                                                                                                      Claim 20; Page 153-158; 1119pp; English
       Kroeger B, Schroeder H,
                                                                                                                                                                                                                                                                                                                                                                                                                   AAB76537 standard; Protein; 1610 AA
                                                                                                                                                                                                                                                                                                                                                       1588 DEPEIGTVGAHLSRRIDEISR 1608
                                                                                                                                                                                                                                                                                                                                         1 DRSNLTRTSGHLSRRSDHLSR 21
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99DE-1031478.
99DE-1031563.
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99DE-1032124.
99DE-1032125.
99DE-1032128.
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                             WPI; 2001-071486/08.
N-PSDB; AAF67749.
                                                                                                                                                                                                                                                                      1610 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200100805-A2.
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         Pompejus M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB76537;
                                                                                                                                                                                                                                                                       Sequence
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AAB76537
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construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B. subtilis rib operon protein translated from reading frame 1.
                                                                                                                                                                                                                                                                                                                                                                                             Haberhauer G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   open reading frame; ORF; structural gene; promoter; Bacillus subtilis; rib operon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.1%; Score 45; DB 22; Length 1610; 42.9%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 253-258; 1119pp; English
                                                                                                                                                                                                                                                                                                                                                                                             Schroeder H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY21801 standard; Protein; 1856 AA.
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99DE-1033005.
99DE-1033006.
99DE-1040764.
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99DE-1042079.
99DE-1042088.
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99DE-1041395.
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99DE-1040831
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Pompejus M, Kroeger B,
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                                                                                                                                                                                                                                                                                                                                                   (BADI ) BASF
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                                                                                                    :666
                                          27'-AUG-1999;
                                                                                                                                            27-AUG-1999;
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03-SEP-1999;
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27-AUG-1
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                                                               27 - AUG -
                                                                                   27-AUG-
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/note= "Encoded by TAA stop codon"
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                                                                                                                  'note=
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                     Misc-difference 110
                                                         Misc-difference 226
                                                                                                                                                                         Misc-difference 266
                                                                                                                                                                                                                                                                                       Misc-difference 289
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                                                                                              Misc-difference 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprises, providing a recombinant bacterium containing an exogenously introduced bacterial ORF (open reading frame) 3 (or ORF5) structural gene and an exogenous promoter, culturing the bacterium, and recovery of the product. The method is useful for the production of large quantities of riboflavin (vitamin B2). Sequences AAY21801-803 are protein sequences AAX21804-806 are protein sequences translated from three different reading frames of B. subtilis rib operon. Reading frames of the complementary sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Riboflavin; rib operon; yeast; bacteria; transformation;
transcription element; gene expression; hair loss; skin inflammation;
growth disorder; vision; vision; sight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                   /note= "residues Xaa are encoded by stop codons"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of bacterial strains for the over production of riboflavin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention relates to a method of producing riboflavin that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 20; Length 1856;
Pred. No. 2.2e+02;
2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2e+02;
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide encoded by rib operon of Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Encoded by TGA stop codon"
                                                                                                                                                                                                                                                                                                                                              Perkins JB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Encoded by TAG stop codon"
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                                                                                                                                                                                                                                                                                                                                            Hermann T,
Location/Qualifiers
1..1856
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89US-0370378.
92US-0873572.
95US-0384626.
98US-0138775.
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L Similarity 55.0%;
11; Conservative
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                                                                                                                                                                                                                                                                                                       VITAMINS INC
                                                                                                                                                                                                                                                                                                                                            Hatch RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 3A-S;
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-418271/35
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                                                                                                                                                                                                                                                                                                                                                              Sloma A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sacillus subtilis
               Misc-difference
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                                                                                                                                                                                                                                                                                                       (HOFF ) ROCHE
                                                                                                                                                   24-AUG-1998;
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                                                                        US5925538-A
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                                                                                                                                                                                                                                1-APR-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY83269;
                                                                                                                                                                                                                                                                                                                                                                Pero JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
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õ a codon" cogon coqou" codon" cogou copon " coqou stop stop stop by TGA stop 'note= "Encoded by TAA stop stop 'note- "Encoded by TAA stop by TAA stop 'note- "Encoded by TAG stop stop note- "Encoded by TAA stop label- Encoded by TGA stop stop 'note= "Encoded by TAA stop stop 'note= "Encoded by TGA stop stop "Encoded by TGA stop note- "Encoded by TGA stop note- "Encoded by TGA stop stop 'note- "Encoded by TAA stop stop "Encoded by TAG stop note- "Encoded by TGA stop by TAA stop 'note= "Encoded by TAA stop by TGA stop note= "Encoded by TAG stop "Encoded by TGA stop "Encoded by TAG stop by TAA stop "Encoded by TAA stop "Encoded by TGA stop by TGA stop by TGA by TAA by TAA by TAA by TAG by TAA by TGA by TAA by TGA by TAG 'note- "Encoded 'note= "Encoded "Encoded "Encoded 'note= "Encoded 'note= "Encoded "Encoded "Encoded "Encoded "Encoded note= "Encoded "Encoded "Encoded 'note= "Encoded 'note- "Encoded "Encoded

	948 /note= 958 /note= 974 /note= 1007 /note= 1019	"Encoded "Encoded	r Aq	TAG	stop	coqou "	
difference difference difference difference difference difference difference	8 ote= 5 ote= 07 ote= 039	"Encoded	, by		•		
	5 ote= 07 07 08 09 ote=	"Encoded	;	TAG	stop	. coqon	•
difference 1 difference 1 difference 2 difference 2	4 ote= ote= ote=		ζq	TAA	stop	codon"	
	ote= 0139 016= 41	"Encoded	bу	TAG	stop	codon"	
. /	ote=	"Encoded	ρλ	TGA	stop	codon"	
·///-	10	"Encoded	рy	TAA	stop	codon"	
/ / / /	081	"Encoded	ρλ	TAG	stop	codon"	
' '	note	"Encoded	ъў	TGA	stop	codon"	
- directored 1	note-	"Encoded	þУ	TGA	stop	codon"	
-/-	note= 138	"Encoded	ρλ	TGA	stop	codon"	
/ difference 1	note=	"Encoded	λą	TAA	stop	codon"	
difference 1	note=	"Encoded	ρλ	TGA	stop	codon"	
difference 1	note= 153	"Encoded	ρλ	TGA	stop	codon"	
-difference 1	note=	"Encoded	ρλ	TGA	stop	codon"	
difference 1	note=	"Encoded	þλ	TAG	stop	codon"	٠
/ /	note=	"Encoded	$_{\rm by}$	TGA	stop	"noboo	
1 \-	note=	"Encoded	þλ	TGA	stop	codon"	
' \-	note=	"Encoded	$\rm by$	TAA	stop	. "uopoo	
, ,,	note=	"Encoded	$\mathbf{p}\mathbf{y}$	TAA	stop	codon"	
, ,-	note=	"Encoded	þλ	TAG	stop	codon"	
1 \	note=	"Encoded	рy	TGA	stop	codon"	
' \	note=,	"Encoded	$\mathbf{p}\mathbf{y}$	TGA	stop	codon"	
difference 1	note=	"Encoded	ρλ	TGA	stop	codon"	
difference 1	note=	"Encoded	$\dot{\rm by}$	TAG	stop	codon"	
difference 1	note=	"Encoded	ρλ	TAA	stop	codon"	
/difference 1	note=	"Encoded	ρλ	TAA	stop	codon"	
difference 1	note=	"Encoded	ρλ	TGA	stop	codon"	
-difference	/note=	"Encoded	ρλ	TGA	stop	codon"	
difference 1	note	"Encoded	ρλ	TGA	stop	"uopoo	
difference 1	note=	"Encoded	ρλ	TGA	stop	codon"	
-difference	note=	"Encoded	γq	TGA	stop	. "uopoɔ	
difference '	note=	"Encoded	bγ	TGA	stop	codon"	
difference 1	note=	"Encoded	ρλ	TGA	stop	codon"	
' -	note=	"Encoded	by	TGA	stop	codon"	
- \-	note=	"Encoded	ρλ	TGA	stop	codon"	

Gaps Zinc finger; DNA binding; Cys2-His2 class; 5-methylcytosine; meC; diagnostic; detection; chimera. ö Score 45; DB 21; Length 1856; Pred. No. 2.2e+02; 2; Mismatches 7; Indels 0 /note= "Encoded by TAA stop codon" Misc-difference 1808 'note= "Encoded by TGA stop codon" 'note= "Encoded by TAA stop codon" /note= "Encoded by TGA stop codon" Misc-difference 1645 /note= "Encoded by TAA stop codon" 1659 /note= "Encoded by TGA stop codon" 1776 /note= "Encoded by TAA stop codon" /note= "Encoded by TAA stop 1628 /note= "Encoded by TAA stop Misc-difference 1684 'note= "Encoded by TGA stop <u>ι.</u> Zinc finger clone zfHHA(Y) peptide. (HOFF) HOFFMANN LA ROCHE & CO AG AAY33370 standard; peptide; 21 AA. 11 | |:| || || || || || || || || || 385 DRPNPIRSSALLSXRTDKLS 404 1 DRSNLTRTSGHLSRRSDHLS 20 Perkins JB, Pero JG, Sloma A; 98GB-0005576. 98GB-0006895. 98GB-0007246. Query Match 42.1%; Best Local Similarity 55.0%; Matches 11; Conservative (MEDI-) MEDICAL RES COUNCIL. 99EP-0124888 89US-0370378 90EP-0111916 99WO-GB00816 01-DEC-1999 (first entry) Misc-difference 1537 Misc-difference 153 WPI; 1999-562106/47 Choo Y, Isalan M; Misc-difference Misc-difference Misc-difference 17-MAR-1998; 31-MAR-1998; 03-APR-1998; 17-MAR-1999; EP1001026-A2 22-JUN-1990; 22-JUN-1989; 22-JUN-1990; Unidentified WO9947656-A2 23-SEP-1999. 17-MAY-2000 AAY33370; ò g

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New zinc finger polypeptides that bind DNA containing modified bases, used as diagnostic and research reagents and for regulating gene transcription

Example 4; Page 36; 56pp; English.

This invention describes a novel zinc finger (ZF) polypeptide (I) that binds to a target DNA sequence (II) containing a modified base but not to an otherwise identical sequence containing the equivalent unmodified base. The invention also describes methods for preparing a DNA-binding base. The invention also describes methods for preparing a DNA-binding containing a 5-methylcytosine (meC) residue. (I) are used as diagnostic reagents (for detecting modified nucleic acids in complex mixtures, including differentiation of single-base modifications), in research and to produce chimeras, e.g. by fusion to a catalytic domain of a centralition express (the product can then cleave only modified DNA), or to a DNA cleavage or activating domain (to give products that can regulate gene transcription, by sequence-specific cleavage or activation, dependent on presence of a modified base). (I) recognize modified bases in preference to unmodified ones, in a sequence-dependent manner, so have extremely high specificity. This sequence repercents a zinc finger clone peptide fragment described in the method of the invention.

21 AA; Sequence

Gaps ; 0 Score 44; DB 20; .Length 21; Pred. No. 1.8; 2; Indels 1; Mismatches 2; Indels Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative

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9 SGHLSRRSDHLS 20

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2 SDELTRRSDHLS 13

Search completed: July 15, 2003, 16:32:41 Job, time : 70 secs.

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 15, 2003, 16:30:06; Search time 15 Seconds (without alignments) 134.588 Million cell updates/sec

SEQ55-247-68 107 1 DRSNLTRTSGHLSRRSDHLSR 21 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable requiator	hypothetical prote		pX-tax-orf II (alt	dnoo	transfer protein T	traY protein - Esc	L-aspartate oxidas	hypothetical prote	isocitrate lyase (isocitrate lyase	sensory histidine	transformer-2 sex-	transformer-2 prot	(4	glycine-tRNA ligas		transcription regu	hypothetical prote			0	L-aspartate oxidas	hypothetical prote					
SUMMAKIES	ID	F45714	D61547	E45714	C46181	T15555	D37390	BVECRY	E81780	AD1857	T07632	T07631	T06353	WZCNIU	WZCSI	WZRPI	S53505	A84229	D35846	A32373	A31638	C71296	S25563	A84248	н71700	B83412	S55114	н81203	AF0330	F84430
	DB	7	~	7	7	7	~	Н	7	~	N	~	7	Н	Н	-	?	~	7	~	7	٦	7	~	~	7	ď	7	7	7
	Length	87	87	240	241	328	71	75	502	692	557	558	575	576	576	576	576	542	136	256	264	462	1122	213	226	425	462	205	. 545	608
dР	Query	50.5				٠	43.0	42.1	42.1	٠	41.6		٠	41.6	41.6	•	•	•	40.2	40.2	40.2	•	40.2	39.3	e,	6	ġ.	6	39.3	39.3
	Score		54	54	54	25	46	45	45	45	44.5	٠	44.5	44.5	44.5	44.5	44.5	44	43	43	43	43	43	42	42	42	42	42	42	42
	Result No.	н	7	3	4	S	9	7	80	o	10	11	12	13	14	15	16	17	18	19	20	21	22	. 23	24	25	56	27	28	53

5-aminolevulinate	nuclear pore compl	hypothetical prote	conserved hypothet	gene 22 protein -	M protein precurso	mip-like protein p	probable fkbp-type	heat shock protein	hypothetical prote	conserved hypothet	hypothetical prote	alkaline exonuclea	low molecular weig	transducer-like pr	ribonucleoside-dip
S31846	S42718	T27864	A75527	WZBE22	S61076	S25255	S28638	A45516	G95256	H98121	E30857	T10400	A44841	T45022	WMBY3L
7	7	7	7	Н	7	~	7	~	7	7	~	7	~	7	Т
648	1475	1650	376	2763	95	243	243	266	335	335	424	424	469	580	882
39.3	39.3	39.3	38.8	38.8	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3
42	42	42	41.5	41.5	41	41	41	41	41	41	41	41	41	41	41
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1
	probable regulatory protein pl3 II, alternative splice form - human T-cell lymphotrop C; Species: human T-cell lymphotropic virus type 1, HTLV-1 C; Date: 22-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 23-May-1997 C; Accession: F45714 R; Gasain, A: Hoper: E: Vanadibara, R: Gallo, R C: Franchin; G
	J. Virol. 67, 1015-1023, 1993 A. Tirol. 67, 1015-0026, 1023, 1993 from the complete nucleotide sequence of a highly divergent human T-cell leukemia (ly
	liom Other geographical regions. A;Reference number: A45714; MUID:93124536; PMID:8419636 A;Contents: F45714 A:Accession: F45714
	A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-87 <ges> A;Note: sequence extracted from NCBI backbone (NCBIP:122473)</ges>
	Query Match 50.5%; Score 54; DB 2; Length 87; Best Local Similarity 71.4%; Pred. No. 0.13; Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
	6 TRTSGHLSRRSDHL : :
	Db 46 SRPTGHLSRASDHL 59
	RESULT 2 D61547
	hypothetical protein II (pX region) - human T-cell lymphotropic virus type 1 (isolate C; Species: human T-cell lymphotropic virus type 1, HTLV-1 C; Date: 28-Oct_1994 #sequence_revision 28-Oct-1994 #text_change 08-Oct-1999
	C;Accession: D61247 K;Tsujimoto, A:, Teruuchi, T.; Imamura, J.; Shimotohno, K.; Miyoshi, I.; Miwa, M. Mol. Biol. Med. 5, 29-42. 1988
	A;Title: Nucleotide sequence analysis of a provirus derived from HTLV-1-associated my A;Reference number: A61547; MUID:88232270; PMID:2897612
	A; Status: preliminary A; Molecule type: DNA A; Residues: 1-87 <tsu></tsu>
	A;Cross-references: GB:M37301; NID:g541634; PIDN:AAA45391.1; PID:g541638
	Query Match 50.5%; Score 54; DB 2; Length 87; Best Local Similarity 71.4%; Pred. No. 0.13; Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
	QY 6 TRTSGHLSRRSDHL 19 : :

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Gaps

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Length 328;

DB 2;

seq55-247-68.rpr

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C;Accession: D37390
R;Graus-Goeldner, A.; Graus, H.; Schlacher, T.; Hoegenauer, G.
Plasmid 24, 119-131, 1990
A;Title: The sequences of genes bordering orlT in the enterotoxin plasmid P307: compa A;Reference number: A37390; MUID:91261994; PMID:2096398
A;Accession: D37390
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Escherichia coli
C.Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-71 <GRA>
A;Cross-réferences: GB:M62986; NID:g150463; PIDN:AAA25524.1; PID:g150467
                                                                                                                                                                                                                                                                                                                                                                                                                                                           transfer protein TraY - Escherichia coli plasmid P307
                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2; 3; Mismatches
                                                                                                                                           Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tray protein - Escherichia coli plasmids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DRSNLTRTSGHLSRRSDHLSR 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| |:|: | |||:|
31 DRSGRTKTNEVFIRLKDHLNR 51
                                                                                                                                                                                                                                                                                         | |||||||| | |||
283 NFTRTSGHLLGYSKHL 298
                                                                                                                                        48.68;
68.88;
                                                                                                                                                                                                                                                        4 NLTRISGHLSRRSDHL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                                                               Query Match
Best Local Similarity 68.8'
Matches 11; Conservative
C;Genetics:
A;Gene: CESP:srg-1
A;Map position: 3
A;Introns: 69/3; 190/3; 298/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: traY pro:
C;Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-71 <GRA>
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A; Residues: 1-75 <INA>
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A; Start codon: TTG
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Genome: plasmid
C;Superfamily: ++>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          px-tax-orf II (alternatively spliced) - human T-cell lymphotropic virus type 1
C; Species: human T-cell lymphotropic virus type 1, HTLV-1
C; Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C; Accession: C46181; D46181
R; Koralnik, I.J.; Gessain, A.; Klotman, M.E.; Lo Monico, A.; Berneman, Z.N.; Franchini, Proc. Natl. Acad. Sci. U.S.A. 89, 8813-8817, 1992
A; Title: Protein is foroms encoded by the px region of human T-cell leukemia/lymphotropid A; Reference number: A46181; MUID:92409607; PMID:1528897
A; Statuus: preliminary; not compared with conceptual translation
A; Residues: 1-241 < KOR>
                                         probable regulatory function protein p30 II, alternative splice form - human T-cell lymp C; Species: human T-cell lymphotropic virus type 1, HTLV-1 C: Date: 22-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 23-May-1997 C; Accession. E45714 B; Gesaln, A.; Boeri, E.; Yanagihara, R.; Gallo, R.C.; Franchini, G. J. Virol. 67, 1015-1023, 1993 A; Title: Complete nucleotide sequence of a highly divergent human T-cell leukemia (lympi from other geographical regions. A; Reference number: A45714; MUID:93124536; PMID:8419636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-328 cLAT>
A;Cross-references: EMBL:U00049; NID:9485101; PID:9485105; PIDN:AAC47053.1; GSPDB:GNÖ002
A;Experimental source: strain Bristol N2; clone C18F10
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T15555
R;Latreille, P. Submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C18F10.
A;Reference number: 218369
A;Accession: T15555
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A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-240 <GES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 155-241 <KO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.5%; Score 54; DB 2; Length 241; Best Local Similarity 71.4%; Pred. No. 0.4; Matches 10; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: sequence extracted from NCBI backbone (NCBIP:114307) A;Accession: D46181
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: sequence extracted from NCBI backbone (NCBIP:122472)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: sequence extracted from NCBI backbone (NCBIP:114308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB 2;
Pred. No. 0.4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vuery Match 50.5%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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199 SRPTGHLSRASDHL 212
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200 SRPTGHLSRASDHL 213
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Gaps

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Length 71; Indels

DB 2;

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A; Description: involved in the conjugation process of bacterial cells for the exchang
C:Species: Escherichia coli
C:Species: Escherichia coli
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: C25033; C32014
R;Finlay, B.B.; Frost, L.S.; Paranchych, W.
A:Finlay, B.B.; Frost, L.S.; Paranchych, W.
A;Fitle: Origin of transfer of Incf plasmids and nucleotide sequences of the type II
A;Reference number: A25033; MUID:87008371; PMID:3531163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      traY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Inamoto, S.; Yoshloka, Y.; Ohtsubo, E. J. Bacteriol. 170, 2749-2757, 1988
A; Title: Identification and characterization of the products from the traJ and A; Reference number: A32014; MUID:88227859; PMID:2836369
                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Mosidues: 1-75 FINA
A; Cross-references: GB:M15136; NID:g151788; PIDN:AAA26076.1; PID:g151789
A; Experimental source: plasmid R100-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M20941; NID:g151778; PIDN:AAA26073.1; PID:g151781
A;Experimental source: plasmid R100
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seq55-247-68.rpr

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catalyzes reversible conversion of isocitrate to succinate and glyoxyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Description: catalyzes reversible conversion of isocitrate to succinate and catalymay: glyoxylate bypass C; Superfamily: isocitrate lyase C; Superfamily: isocitrate lyase C; Keywords: carbon-carbon lyase; glyoxylate bypass; glyoxysome; oxo-acid-lyase
                                                isocitrate lyase (EC 4.1.3.1), glyoxysomal - soybean (fragment)
C;Species: Glyoine max (soybean)
C;Species: Glyoine max (soybean)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Apr-2000
C;Accession: T07632
R;Guex, N.; Henry, H.; Widmer, F.
submitted to the EMBL Data Library, August 1993
A;Reference number: 216065
A;Reference number: 216065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isocitrate lyase (EC 4.1.3.1), glyoxysomal - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Apr-2000
C;Accession: T07631
R;Guex, N.; Henry, H.; Widmer, F.
unpublished results 1992, cited by EMBL
A;Reference number: 216064
A;Reference number: 216064
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C;Species: Lycopersicon esculentum (tomato)
C;Dacte: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C;Accession: T06353
R;Janssen, B.J.
Plant physiol. 108, 1339, 1995
A;Fille: A cDNA clone for isocitrate lyase from tomato.
A;Reference number: Z15618; MUID:95357440; PMID:7630969
                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
Andlecule type: mRNA
A;Residues: 1-557 <GUE>
A;Cross-references: EMBL:L02330; NID:g349328; PIDN:AAA33977.1; PID:g349329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-558 <GUE>
A;Cross-references: EMBL:L02329; NID:g349326; PIDN:AAA33976.1; PID:g349327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
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Pred. No. 33;
10; Mismatches
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Pred. No. 33;
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187 DQSSVTKKCGHMAGKVLVAISEHINR 212
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Best Local Similarity 30.8
Matches 8; Conservative
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A;Note: ICL
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A;Gene: ICL
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T07631
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T06353
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A; Note: Nostoc sp.
A; Note: Nostoc sp.
A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C; Accession: AD1857
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, B DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                           L-aspartate oxidase (EC 1.4.3.16) NWA2092 [imported] - Neisseria meningitidis (strain 22 C; Species: Neisseria meningitidis (c) Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C; Accession: EB1780 C; Moule, S.; Mungall, K.; Quall, M.A.; Rajandream, Nature 404, 502-506, 2000 C; Moule, S.; Mungall, K.; Quall, M.A.; Rajandream, A; Raite: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85308.1; PID:g73807:
A;Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics: NMA2092
A;Gene: nadB; NMA2092
C;Superfamily: fumarate reductase flavoprotein; 3-oxosteroid 1-dehydrogenase homology; C;Keywords: oxidoreductase
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-692 KURB
A;Cross-references: GB:BA000019; PIDN:BAB72363.1; PID:g17129750; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all0405
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C;Superfamily: tray protein
C;Keywords: DNA binding; pilin formation; plasmid transfer
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Pred. No. 35;
1; Mismatches
                                                                             Score 45; DB 1;
Pred. No. 3.1;
4; Mismatches
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Pred. No. 24;
3; Mismatches
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ERSGRIKINEVLVRLRDHLNR 51
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Best Local Similarity 45.8%;
Matches 11; Conservative
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ilarity 47.1%;
Conservative
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ilarity 47.6%;
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Best Local Similarity
8; Conserve
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Best Local Similarity
Matches 10; Conserv
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A;Molecule type: DNA
A;Residues: 1-502 <PAR>
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NyAlternate names: isocitrate; isocitratase; isocitritase
C;Specias: Richinus communis var. zanzibarensis (castor bean)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: S06274
R;Beeching, J.R.; Northcote, D.H.
Plant Mol. Biol. 8, 471-475, 1987
A;Title: Nucleic acid (cDNA) and amino acid sequences of isocitrate lyase from castor be A;Reference number: S06274
A;Accession: S06274
A;Molecule type: mRNA
A;Residues: 1-576 CBEE>
A;Molecule type: mRNA
A;Residues: 1-576 CBEE>
A;Cross-references: GB:M17145; NID:g169706; PIDN:AAA53378.1; PID:g169707
C;Comment: This enzyme catalyzes the reversible conversion of isocitrate to succinate and is involved in storage lipid mobilization during the growth of higher plant seedlings.
C;Superfamily: isocitrate lyase
C;Reywords: carbon-carbon lyase; glyoxylate bypass; oxo-acid-lyase
                                             A Molecule type: mRNA
A; Residues: 1-575 < JAN>
A; Residues: 1-575 < JAN>
A; Residues: 1-575 < JAN>
A; Cross-references: EMBL:018678; NID:9624210; PIDN:AAA82738.1; PID:9624211
A; Experimental source: strain UC82B; tissue type first true leaf
C; Function:
A; Description: catalyzes the reversible conversion of isocitrate to succinate and glyoxy
C; Superfamily: isocitrate lyase
C; Keywords: carbon-carbon lyase; glyoxylate bypass; oxo-acid-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-576 <TURN
A; Cross-references: EMBL:X52136; NID:918485; PIDN:CAA36381.1; PID:918486
C; Comment: This enzyme catalyzes the reversible conversion of isocitrate to succinate and is involved in mobilization of sored lipids during the growth of higher plant seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isocitrate lyase (EC 4.1.3.1) - upland cotton
N;Alternate names: isocitratese; isocitratese;
C;Species: Gossyplum hirautum (upland cotton)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: S10771; Arelease, R.N.
Biochim. Biophys. Acta 1049, 223-226, 1990
A;Title: Characterization of a cDNA clone encoding the complete amino acid sequence of A;Reference number: S10771; MUID:90304228; PMID:2194576
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C;Keywords: carbon-carbon lyase; glyoxylate bypass; oxo-acid-lyase
                                                                                                                                                                                                                                                                                                       Length 575;
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                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 30.00
Best Local Similarity 30.00
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Best Local Similarity 30.89
Matches 8; Conservative
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A; Accession: T06353
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Matches
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C;Accession: JQ1105
R;Comai, L.; Dietrich, R.A.; Maslyar, D.J.; Baden, C.S.; Harada, J.J.
Plant Cell 1, 293-300, 1989
A;Title: Coordinate expression of transcriptionally regulated isocitrate lyase and ma A;Reference number: JQ1105; MUID:92393389; PMID:2535504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Molecule type: mRNA
A)Residues: 1-576 <COM>
C)Comment: This enzyme catalyzes the reversible conversion of isocitrate to succinate
is involved in storage lipid mobilization during the growth of higher plant seedling
C;Superfamily: isocitrate lyase
C;Keywords: carbon-carbon lyase; glyoxylate bypass; oxo-acid-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                   isocitrate lyase (EC 4.1.3.1) - rape
N'Alternate names: isocitratase; isocitratase; isocitritase
C'Species: Brassica napus (rape)
C'Species: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 30-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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30.8%; Pred. No. 34;
tive 10; Mismatches
                                 205 DQSSVTKKCGHMAGKVLVAISEHINR 230
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1 DRSNLTRTSGHLSRR-
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

- protein search, using sw model OM protein

Run on:

(without alignments)
37.870 Million cell updates/sec July 15, 2003, 16:29:55 ; Search time 23 Seconds

SEQ55-247-68 107 1 DRSNLTRTSGHLSRRSDHLSR 21

Perfect score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SITMMARTES

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FAMILY

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Gaps

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48.6%; Score 52; DB 1; Length 328; 68.8%; Pred. No. 0.29; ive 0; Mismatches 5; Indels

Query Match 48.6 Best Local Similarity 68.8 Matches 11; Conservative

δ Q RESULT 2 TRY5_ECOLI

POTENTIAL. 3FA9A818CF27EB05 CRC64;

POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL

TRANSMEM TRANSMEM SEQUENCE

T'RANSMEM T'RANSMEM I'RANSMEM

I'RANSMEM

Transmembrane; Multigene family. TRANSMEM 25 45 POI

Pfam; PF02118; Srg; 1. PRINTS; PR00698; IMPROTEINSRG

EMBL; U00049; AAC47053.1; "WormPep; C18F10.4; CE00781. InterPro; IPR000609; Srg.

	•	Description	P46570 caenorhabdi	Q00736 escherichia	-	-		Q9se26 dendrobium				P93110 cucurbita m		P17069 gossypium h			P19018 drosophila				Q04235 saccharomyc	P38092 emericella	P49790 homo sapien	_	P09278 varicella-z	P26623 chlamydia t	_	_	P21672 saccharomyc	P21524 saccharomyc	Q9h2x6 homo sapien		-	P19019 gallus gall	P01029 mus musculu
SUMMARIES		QI	SRG1_CAEEL	TRY5_ECOLI	TRY3_ECOLI	ACE2_SOYBN	ACE1_SOYBN	ACEA_DENCR	ACEA_LYCES	ACEA_ARATH	ACEA_BRANA	ACEA_CUCMA	ACEA_CUCSA	ACEA_GOSHI	ACEA_RICCO	RL36_TRIHM	TRA2_DROME	SYG_TREPA	RPOB_THECE	UPPS_RICPR	YMA5_YEAST	HEM1_EMENI	N153_HUMAN	BP28_CAEEL	TEGU_VZVD	MIP_CHLTR	EXON_NPVOP	XNIF_XENLA	RIR3_YEAST	RIR1_YEAST	HIK2_HUMAN	TROP_HUMAN	YPPC_CHLLI	GAB3_CHICK	CO4_MOUSE
		igth DB	328 1	71 1		557 1		574 1	575 1	576 1	576 1	576 1	576 1	576 1	576 1	105 1	264 1	462 1	122 1	226 1	462 1	648 1	475 1	.650 1	763 1	243 1	424 1	470 1	869 1	888 1	1198 1	.387 1	203 1	476 1	738 1
æ	Query	Match Length	48.6	43.0	•	9.	9.	9.						9.	9.		۲.	0.5	۲.		۳.	m.	9.3	e. 6	8.8		m.	ж •	ъ.	۳.	m	38.3	37.4	37.4	37.4
		Score	52	46	45	44.5	44.5	44.5	44.5	4	4	44.5	44.5	4	44.5	43	43	43		42	42	42	42	4	41.5	41	41	41	41	41	41	41	40	40	40
	Result	NO.	ч	7	٣	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33

	046378 oryctolagus Q9ttb4 sus scrofa Q9pjk1 chlamydia m	. 0927p3 chlamydia p . 006828 homo sapien P50608 mus musculu				•		e) ate)	protein).	Jaenorhabditis elegans. Sukaruota, Matanoa, Namatoda, Chromadorna, Bhahditida, Bhahditoidea.	Miabatetaa, Miabateataa,				Latrellie F.; Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.	SUBCELLULAR LOCATION: Integral membrane protein (Probable).	SIMILLARITY: BELONGS TO THE C.ELEGANS RECEPTOR-LIKE PROTEIN SKG
V51K_ACLSA	FMOD_RABIT LUM_PIG MIP_CHLMU	MIP_CHLPN FMOD_HUMAN FMOD_MOUSE	FMOD_RAT	SYG_YEAST SYTC_SCHPO LKA3 PASHA	ALIGNMENTS		PKI;	32, Last sequence update) 41, Last annotation update)	Serpentine receptor class gamma 1 (Srg-1 protein) SRG-1 OR C18F10.4.	o. Chromadoroa	Rhabditidae, Peloderinae, Caenorhabditis.				EMBL/GenBank/	ntegral membra	THE C.ELEGANS
457		258 376 376	376 607	667 703 953			SIANDAKD; [Rel. 32, Created)		eptor class g 0.4.	elegans.	eloderinae; C		N.A.	N2;	-1994) to the	R LOCATION: I	: BELONGS IO
39.5	5 5 5 6 6 6 6	<i>.</i>	56 6 6 8	5 5 5 5 6 6 6		1 AEEL Poli Caper		01-NOV-1995 (R	Serpentine recepto SRG-1 OR C18F10.4.	Caenorhabditis elegans. Bukarmota, Metaroa, Nem	habditidae; P	WCBI_TaxID=6239;	SEQUENCE FROM N.A.	STRAIN-Bristol N2;	Jubmitted (MAY	-! - SUBCELLULA	
ю с 41	355	w w 4 ∞ w 0	4.1	4 4 4 E 4 7		RESULT 1 SRG1_CAEEL				SO		N XO			R 18		

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RESULT 4
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J. Bacteriol. 168:132-139(1986).
                                                                                                                                                                                                                                                                                                                                                                                       BACTERIAL CELLS
                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
Plasmid IncFII R100-1, and Plasmid IncFII R100.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.0%; Score.46; DB 1; Length 71;
47.6%; Pred. No. 0.48;
ive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid; Conjugation; DNA-binding.
SEQUENCE 71 AA; 8103 MW; 9A031E0ECBE99263 CRC64;
                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
 71 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 AA
 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLASMID-IncFII R100-1;
MEDLINE-87008371; PubMed-3531163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M62986; AAA25524.1; -.
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Best Local Similarity 47.6'
Matches 10; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                   Plasmid IncFI P307
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                                                                                                                                 Escherichia coli
                                                                                                                                                                                                             NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=562;
                                                                                             TraY protein.
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                                                                                                                                                                                         Escherichia
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TRY5_ECOLI
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                  MEDLINE-88227859; PubMed-2836369; Inamoto S. Yoshioka Y., Ohtsubo E.; Identification and characterization of the products from the trajand tray genes of plasmid R100."

J. Bacteriol. 170:2749-2757(1988).

I-CHURTION: INVOLUED IN THE CONJUGATION PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA. IT IS ALSO RESPONSIBLE FOR CONJUGAL DNA METABOLISM. TRAY IS REQUIRED FOR STRAND-SPECIFIC.

NICKING AT ORIT, THE TRANSPER ORIGIN.

I-SIMILARITY: TO TRAY PROTEIN OF OTHER PLASMIDS.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Isocitrate lyase 2 (EC 4.1.3.1) (Isocitrase 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid; Conjugation; DNA-binding.
SEQUENCE 75 AA; 8542 MW; 88D4B04C4B5DE07A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 1;
Pred. No. 0.74;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-cv. Maple Arrow; TISSUE-Cotyledon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M15136; AAA26076.1; -. EMBL; M20941; AAA26073.1; -.
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Best Local Similarity 47.6
Matches 10; Conservative
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PIR; C32014; C32014.
PLASMID-IncFII R100;
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P45457;
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ACEA_LYCES
ID ACEA_LN
AC P49297
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                             Matches
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or send an.email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papillionoideae; Phaseoleae; Glycine.
NCBL_TaxID=3847;
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
MICROBODY TARGETING SIGNAL (POTENTIAL).
9985CA5EA24F5DDB CRC64;
                                                                                               BY SIMILARITY.
MICROBODY TARGETING SIGNAL (POTENTIAL),
486D5CE420B7AD95 CRC64;
      Interpro; IRR00018; Isocit_lyase.

Interpro; IRR00018; Isocit_lyase.

Probom; PR001857; ISOcit_lyase; 2.

PROSITE; PS00161; ISOCITRATE_LYASE; 1.

PROSITE; PS00342; MICROBODIES_CTER; 1.

Glyoxylate bypass; Tricarboxylic acid cycle; Lyase; Glyoxysome; Multigene family.

NON_TER.

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01-NOV-1995 (Rel. 32, Last annotation update)
Isocitrate lyase 1 (EC 4.1.3.1) (Isocitrase 1) (Isocitratase 1)
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                                                                                                                                       41.6%; Score 44.5; DB 1; Length 557; 30.8%; Pred. No. 9.3;
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                                                                                                                                                                                                                                                  558 AA.
                                                                                                                                                         10; Mismatches
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DOSSVTKKCGHMAGKVLVAISEHINR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfan; PF00463; ICL; 1.
Prodom; PD001857; Isocit_lyase; 2.
PROSITE; PS00161; ISOCITRATE_LYASE; 1.
PROSITE; PS00342; MICROBODIES_CTER; 1.
                                                                                                                                                                            1 DRSNLTRTSGHLSRR----SDHLSR 21
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISSP; P28298; 1DQU.
.nterPro; IPR000918; Isocit_lyase.
                                                                                                                                                                                                                                       62840 MW;
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EMBL; L02330; AAA33977.1;
                                                                                                                                                         Conservative
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195
557
                                                                                                                                                                                                                                                                                                                                 Glycine max (Soybean).
                                                                                              195 1
555 5
557 AA;
                                                                                                                                                                                                                                                                                                             (ICL 1) (Fragment).
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                                                                                                                                                Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family.
                                                                                              ACT_SITE
SITE
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ACT_SITE
SITE
                                                                                                                  SEQUENCE
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                                                                                                                                       Query Match
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                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- CATALITIC ACTIVITY: ISOCILITATE = SUCCIDATE + 91yoxylate.
-i- PATHWAY: FIRST STEP IN GLYOXXLATE BYPASS, AN ALTERNATIVE TO THE TRICARBOXYLIC ACID CYCLE (IN BACTERIA, PLANTS, AND FUNGI).
-i- SUBUNIT: HOMOTETRAMER (BY SIMILLARITY).
-i- SUBCELLULAR LOCATION: Glyoxysomal.
-i- DEVELOPMENTAL STAGE: EXPRESSED MAXIMALLY DURING POSTGERMINATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MICROBODY TARGETING SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Epidendroideae; Dendrobieae; Dendrobiinae;
                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1socitrate lyase (EC 4.1.3.1) (Isocitrase) (Isocitratase) (ICL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Vellupillai M., Goh C.-J., Swarup S.;
Sequence analysis of DcrIcl, an isocitrate lyase gene from the tropical orchid, Dendrobium crumenatum.";
(In) Plant Gene Register PGR99-178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000518; Isocit_lyase.
Pfam; PF00463; ICL; 1.
Probom: PP001187; ISocit_lyase; 2.
PROSITE; PS00161; ISOCITRATE_LYASE; 1.
PROSITE; PS00342; MICROBODIES; CTER; 1.
Glyoxylate bypass; Tricarboxylic acid cycle; Lyase; Glyoxysome.
ACT_SITE 212 212 212
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Length 558;
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DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dendrobium crumenatum (Tropical pigeon orchid).
                                                                                                                                                                                                                                                                                   574 AA.
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                30.8%; Preu. ...
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Score 44.5;
                                                                                                                                   187 DQSSVTKKCGHMAGKVLVAISEHINR 212
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                                                                                                  1 DRSNLTRTSGHLSRR----SDHLSR
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41.68;
                                                 Conservative
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                     Best Local Similarity
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P49297;
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Query Match
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NCBI_TaxID=3708;
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Best Local
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                                                                                                                                                                                                                                                           eudicots; Rosidae;
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573 575 MICROBODY TARGETING SIGNAL (POTENTIAL).
575 AA; 64720 MW; F398FA96C7110B4E CRC64;
01-FEB-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Isocitrate lyase (EC 4.1.3.1) (Isocitrase) (Isocitratese) (Isocitr
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosiceurosids II; Brassicales; Brasslcaceae; Arabidopsis.
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STRAIN=cv. Columbia;
MEDLINE=20277480; PubMed=10819329;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACEA_ARATH STANDARD; PRT; 576 AA.
P28297; 041948 09L522;
01-DEC-1992 (Rel. 24, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1socitrate lysse (EC 4.1.3.1) (Isocitrase) (Isocitratase) (ICL).
ICL OR AT3G21720 OR MSD21.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00463; ICL; 1.
ProDom; PB00463; ICL; 1.
PROSITE; PS00161; ISOCITRATE LYASE; 1.
PROSITE; PS00342; MICROBODIES_CTER; 1.
GIyoxylate bypass; Tricarboxylic acid cycle; Lyase; Glyoxysome.
ACT_SITE 213 PROBABLE.
STR 573 575
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                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-cv. UC82B; TISSUE-Leaf;
MEDLINE-95357440; PubMed-7630969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U18678; AAA82738.1; -. HSSP; P28298; 1DQU.
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                                                                                                                                                                                                                                                   Janssen B.J.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
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MEDLINE=92393389; PubMed=2535504;
MEDLINE=92393389; PubMed=2535504;
Medline=10, Dietrich R.A., Maslyar D.J., Baden C.S., Harada J.J.;
"Coordinate expression of transcriptionally regulated isocitrate lyase and malate synthase genes in Brassica napus L.";
Plant Cell 1:293-300(1989).
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P25248; 004910;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Isocitrate lyase (EC 4.1.3.1) (Isocitrase) (Isocitratese) (ICL).
"Structural analysis of Arabidopsis thaliana chromosome 3. T. Se
features of the regions of 4,504,864 bp covered by sixty Pl and
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QQMV -> PLTC (IN REF. 2).
528F15CE04DD4A87 CRC64;
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PROSITE; PS00161; ISOCITRATE_LYASE; 1.
Glyoxylate bypass; Tricarboxyllc acid cycle; Lyase; Glyoxysome.
ACT_SITE 213 213 PROBABLE.
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                                                                                                                                                                                     Bernhard W.R., Matile P.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: Glyoxysomal.
-i- SIMILARITY: BELONGS TO THE ISOCITRATE LYASE FAMILY.
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Pfam; PF00463; ICL; 1.
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                                                                                                                                                         SEQUENCE OF 1-455 FROM N.A.
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                                                                 clones.";
DNA Res. 7:131-135(2000).
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576 AA;
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8; Conserv
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[1]
SEQUENCE FROM N.A.
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P49296;
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                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last sequence update)
Socitrate lyase (EC 4.1.3.1) (Isocitrase) (Isocitratase) (ICL).
BUNARYOLA: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                MEDLINE-93241152; PubMed-8479425; Zhang J.Z., Gomez-Pedrozo M., Baden C.S., Harada J.J.; Two classes of isocitrate lyase genes are expressed during late embryogeny and postgermination in Brassica napus L."; Mol. Gen. Genet. 238:177-184(1993).
                                                                                                                                                                                                                                                                                                                                                                                   Tricarboxylic acid cycle; Lyase; Glyoxysome.
213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                               A -> V (IN REF. 3).
D -> G (IN REF. 3).
S -> P (IN REF. 3).
S -> N (IN REF. 3).
N -> T (IN REF. 3).
N -> T (IN REF. 3).
W, B1A87701A4ACC350 CRC64;
                                                                                                                                                                                                   -! - SIMILARITY: BELONGS TO THE ISOCITRATE LYASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 DQSSVTKKCGHMAGKVLVAVSEHINR 230
                                                                                                                                                                                                                                                                                                                                                                                                        MICROBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                      ProDom; PD001857; ISOCIT_lyase; 2.
PROSITE; PS00161; ISOCITRATE_LYASE; 1.
PROSITE; PS00342; MICRÒBODIES_CTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DRSNLTRTSGHLSRR----SDHLSR 21
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                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000918; Isocit_lyase.
Pfam; PF00463; ICL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64325 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.6%;
                                                                                                                                                                                                                                                                                                         EMBL; Y13356; CAA73792.1; -. PIR; JQ1105; WZRPI.
HSSP; P28298; 1DQU.
                                                                                                                                                                                                                                                                                                EMBL; L08482; AAA32992.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              213
576
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                              344
576 AA;
                                                                                                                                                                                                                                                                                                                                                                                    Glyoxylate bypass;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eurosids I; Cucu:
NCBI_TaxID=3661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACEA_CUCMA
P93110;
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SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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                                                                                                           cotyledons.";
plant Call Physiol. 37:941-948(1996).
plant Call Physiol. 37:941-948(1996).
-! FUNCTION: INVOLVED IN STORAGE LIPID MOBILIZATION DURING THE GROWTH
OF HIGHER PLANT SEEDLING.
-!- CATALTITE ACTIVITY: ISOCILEAE —: SUCCINATE HYPOXYLATE.
-! PATHWAY: FIRST STEP IN GLYOXXLATE BYPASS, AN ALTERNATYPE TO THE
TRICARBOXYLIC ACID CYCLE (IN BACTERIA, PLANTS, AND FUNGI).
-! SUBDINIT: HOMOTERTAKER (BY STMILARTY).
-! SUBCELLULAR LOCATION: Glyoxysomal.
-! SUBCELLULAR LOCATION: Glyoxysomal.
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MEDLINE=95201243; PubMed=7894014;
Reynoline=95201243; PubMed=7894014;
Reynoline=95201243; PubMed=7894014;
Reynoline=95201243; PubMed=7894014;
The isocitrate lyase gene of cucumber: isolation, characterisation and expression in cotyledons following seed germination.";
Plant Mol. Biol. 27.4874950;
-!- FUNCTION: INVOLVED IN STORAGE LIPID MOBILIZATION DURING THE GROWTH
OF HIGHER PLANT SEEDLING.
-!- CATALYTIC ACTIVITY: Isocitrate = succinate + glyoxylate.
-!- PATHWAY: FIRST STEP IN GLYOXYLATE BYPASS, AN ALTERNATIVE TO THE TRICARBOXYLIC ACID CYCLE (IN BACTERIA, PLANTS, AND FUNCI).
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
MEDLINE-97134001; PubMed-8979395;
Mano S., Hayashi M., Kondo M., Nishimura M.;
"cDNA cloning and expression of a gene for isocitrate lyase in pumpkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MICROBODY TARGETING SIGNAL (POTENTIAL).
269D93D4F13B5990 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
61-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Isocitrate lyase (EC 4.1.3.1) (Isocitrase) (ISOCITRATES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glyoxylate bypass; Tricarboxylic acid cycle; Lyase; Glyoxysome.
ACT_SITE 213 213 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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30.8%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 9.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probon; P0001857; Isocit_lyase; 2. PROSITE; PS00161; ISOCITRATE_LYASE; 1. PROSITE; PS00342; MICROBODIES_CTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DRSNLTRTSGHLSRR-----SDHLSR 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000918; Isocit_lyase. Pfam; PF00463; ICL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cucumis sativus (Cucumber).
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8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 AA;
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seq55-247-68.rsp

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Probom: PD001857; Isocit_lyase; 2.
PROSITE; PS00161; ISOCITRATE_LYASE; 1.
PROSITE; PS00342; MICROBODIES_CTER; 1.
Glyoxylate bypass; Tricarboxylacacid cycle; Lyase; Glyoxysome.
ACT_SITE 213 213 PROBABLE.
SITE 574 576 MICROBODY TARGETING SIGNAL (POTENTIAL).
       InterPro; IPR000918; Isocit_lyase.
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ACEA_RICCO
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                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-AUG-1990 (Rel. 15, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
10-Colstrate lyase (EC 4.1.3.1) (Isocitrase) (Isocitratese)
Gossypium hirsutum (Upland cotton)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       574 576 MICROBODY TARGETING SIGNAL (POTENTIAL).
576 AA: 64611 MW; 717D30B83CD81D6C CRC64;
                                                                                                                                                                                                                                                                                                                 Pfam; PF00463; TCL; 1.
ProDom; PD001857; ISocit_lyase; 2.
PROSITE; PS00161; ISOCITRATE_LYASE; 1.
PROSITE; PS00342; MICROBODIES_CTER; 1.
Glyoxylate bypass; Tricarboxylic acid cycle; Lyase; Glyoxysome.
ACT_SITE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
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SIMILARITY: BELONGS TO THE ISOCITRATE LYASE FAMILY.
                       SIMILARITY: BELONGS TO THE ISOCITRATE LYASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.6%; Score 44.5; D
30.8%; Pred. No. 9.7;
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 DQSSVTKKCGHMAGKVLVAVSEHINR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DRSNLTRTSGHLSRR----SDHLSR 21
SUBCELLULAR LOCATION: Glyoxysomal
                                                                                                                                                                                                                                                                                            InterPro; IPR000918; Isocit_lyase.
                                                                                                                                                                                                                                                    EMBL; Z35499; CAA84632.1; -. HSSP; P28298; 1DQU.
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PIR; S10771; WZCNIU.
HSSP; P28298; 1DQU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 41.6
Best Local Similarity 30.8
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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P17069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBUNIT: HOMOTETRAMER.
-i- SUBCELLULAR LOCATION: Glyoxysomal.
-i- SIMILARITY: BELONGS TO THE ISOCITRATE LYASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beeching J.R., Northcote D.H.; "Nucleic acid (cDNA) and amino acid sequences of isocitrate lyase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unanyous; Viridiplantae; Stréptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                   Gaps
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574 576 MICROBODY TARGETING SIGNAL (POTENTIAL).
576 AA: 64751 MW: 8177A7679050579B CRC64;
                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
1socitrate lyase (EC 4-13.1) (Isocitrase) (Isocitratase) (ICL).
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InterPro; IPM000918; Isocit_lyase.

Probon; PP001657; ISocit_lyase; 2.

PROSITE; PS00161; ISOCITRATE_LYASE; 1.

PROSITE; PS00161; ISOCITRATE_LYASE; 1.

ROSITE; PS001842; MICROBODIES_CTER; 1.

Glyoxylate bypass; Tricarboxylic acid cycle; Lyase; Glyoxysome.

ACT_SITE 213 PROBABLE.

SITE 574 = 7.2
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                                                DB 1; Length 576;
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SEQUENCE 576 AA; 64733 MW; 84D211AA3DCE8700 CRC64;
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                                                                                                                                                                                                                                                                                                                       576 AA.
                                                41.6%; Score 44.5; Di 30.8%; Pred. No. 9.7;
                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Mismatches
                                                                                                                                                                             205 DQSSVTKKCGHMAGKVLVAVSEHINR 230
                                                                                                                                            1 DRSNLTRTSGHLSRR----SDHLSR 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DRSNLTRTSGHLSRR----SDHLSR 21
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                                                                                           10;
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                                                                                                 Conservative
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Best Local Similarity 30.8%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                       STANDARD;
                 Query Match
Best Local Similarity
8; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-89077531; PubMed-3144434;
Amrein H., Gorman M., Noethiger R.;
"The sex-determining gene tra-2 of Drosophila encodes a putative RNA binding protein.";
Cell 55:1025-1035(1988).
                                                                                                                                                                                                                                                                              Fekete C., Posta K., Hornok L.; "Isolation and characterization of a Trichoderma hamatum ribosomal protein gene, TRP36."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: BELONGS TO THE L36E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Trichoderma.
NCBI_TaxID-49224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.2%; Score 43; DB 1; Length 105; 46.7%; Pred: No. 2.4; 1ve 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 AA; 11835 MW; 6C68DB611ED7F620 CRC64;
                                                                                                                            15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
608 ribosomal protein L36 (TRP36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-UUN-2002 (Rel. 41, Last annotation update)
Transformer-2 sex-determining protein.
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            DOSSVTKKCGHMAGKVLVAISEHINR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF308443; AAG28787.1; -.
InterPro; IPR000509; Ribosomal_L36e.
Prom: PF01158; Ribosomal_L36e; 1.
Profom: PD009192: Ribosomal_L36e; 1.
PROSITE; PS01190; RIBOSOMAL_L36E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
SEQUENCE FROM N.A., AND FUNCTION
                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RSNLTRTSGHLSRRS 16
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KPRVSRTKGHLSKRT 41
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nes 7; Conservative
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                                                                                      STANDARD;
                                                                                                                                                                                           Trichoderma hamatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribosomal protein.
                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                             OR P36.
                                                                                 RL36_TRIHM
Q9HFR7:
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P19018;
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            205
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ERRATUM.
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TRA2_DROME
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Matches
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MEDLINE-94170373; PubMed-8124712;
Amrein H., Hedley M.L., Maniatis T.;
"The role of specific protein-RNA and protein-protein interactions in
positive and negative control of pre-mRNA splicing by Transformer 2.";
Cell 76:735-746(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lynch K.W., Maniatis T.; "Synergistic interactions between two distinct elements of a regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in males
in male
                                                                                  SECUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-91006062; Pubmed-2120049;
Amrein H., Maniatis T., Noethiger R.;
"Alternatively spliced transcripts of the sex-determining gene tra-2 of Drosophila encode functional proteins of different size.";
EMBO J. 9:3619-3629(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                transformer-2 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVATION AND REPRESSION OF ALTERNATIVE SPLICING.
ALTERNATIVE PRODUCTS: 4 isoforms; Tmaj/major/A (shown here),
Tmin/minor/B, msTmaj/C and msTmin/D; are produced by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [6]
IDENTIFICATION OF A TRA-2 BINDING SITE IN PRE-MRNA.
MEDLINE-91235294; PubMed=1674449;
Hedley M.L., Maniatis T.;
"Sex-specific splicing and polyadenylation of dsx pre-mRNA requires sequence that binds specifically to tra-2 protein in vitro.";
Cell 65:579-586(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    germ cells.

OWAIN: THE RS2 (ARG/SER-RICH DOMAIN 2) AND RNP-CS
(RIBONUCLEOPROTEIN CONSENSUS, SEQUENCE) DOMAINS ARE REQUIRED FOR BOTH WALE STERLLITY AND FEMALE-SPECIFIC DSX SPLICING BUT THE RS1 DOMAIN IS DISPENSABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goralski T.J., Edstroem J.-E., Baker B.S.; The sex determination locus transformer-2 of Drosophila encodes polypeptide with similarity to RNA binding proteins."; Cell 56:1011-1018(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION OF A PURINE-RICH ENHANCER IN THE ENHANCER COMPLEX MEDLINE-95172379; PubMed-7867927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: Isoforms Tmaj and Tmin are expressed and females. Isoforms msTmaj and msTmin are present only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tian M., Maniatis T.;
A splicing enhancer complex controls alternative splicing
analyses pre-miNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION OF STRUCTURAL DOMAINS, AND MUTAGENESIS.
                                                                                                                                                                                                                                                                                                                  FUNCTION, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICTI
TISSUE=Imaginal disks;
MEDLINE=90337316; PubMed=2116360;
Mattox W., Palmer M.J., Baker B.S.;
"Alternative splicing of the sex determination gene sex-specific in the germ line but not in the soma.";
Genes Dev. 4:789-805(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH SR PROTEINS IN THE ENHANCER COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [5] SEQUENCE OF 9-264 FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89168430; PubMed-2493992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93327418; PubMed-8334698;
Amrein H., Gorman M., Noethiger
Cell 58:420-420(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             doublesex pre-mRNA.";
Cell 74:105-114(1993).
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seq55-247-68.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISSING: IN A36; LOSS OF FEMALE-SPECIFIC
DSX SPLICING; AND MALE FERTILITY.
SPLICING; AND MALE FERTILITY.
F->A: IN PMJ; NOS OF FEMALE-SPECIFIC DSX
SPLICING; AND MALE FERTILITY.
F->A: IN PM2; NO FEMALE-SPECIFIC DSX
SPLICING; SOME LOW MALE FERTILITY.
SPLICING; SOME LOW MALE FERTILITY DSX
SPLICING, LOSS OF MALE FERTILITY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQRAHTPTPGVYLGRQPRGKAPRSFSPRRGRRVYHDRSASP
YDNYRDRYDYRNDRYDRNLRRSPSRNRYTRNRSYSRSRSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORSRGFCFIYFEKLSDARAAKDSCSGIEVDGRRIRVDFSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSX SPLICING AND MALE FERTILITY.
S->F: IN A15, LOSS OF FEMALE-SPECIFIC DSX
SPLICING AND MALE FERTILITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3->T: IN PM4; LOSS OF FEMALE-SPECIFIC DSX
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEXUAL differentiation; Permatogenesis; RNA-binding; mRNA splicing; Alternative splicing; Phosphorylation.

DOMAIN 21 90 ARG/SER-RICH (RRI)

DOMAIN 176 196 LINKER.

DOMAIN 177 264 ARG/SER-RICH (RS2 DOMAIN).

VARSPLIC 1 85 MISSING (IN ISOPORM TWIN).

WARSPLIC 2 39 MISSING (IN ISOPORM TWIN).

VARSPLIC 2 406 TORSRGFCFIYFEKLSDARAAKDSCSGIEVDERRIPUDFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEMPERATURE-SENSITIVE PHENOTYPE.
MISSING: IN D5; LOSS OF FEMALE-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING: IN D4; LOSS OF FEMALE-SPECIFIC DSX SPLICING, GREATLY REDUCED MALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRRTSSRY -> INP (IN ISOFORM MSTMIN).
MISSING: IN D2; GREATLY REDUCED FEMALE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIFIC DSX SPLICING.
MISSING: IN D1; GREATLY REDUCED FEMALE-
SPECIFIC DSX SPLICING, RETAINS MALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S->A: IN PM3; GREATLY REDUCED FEMALE-
SPECIFIC DSX SPLICING, RETAINS MALE
FERTILITY AND TEMPERATURE-SENSITIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPLICING, RETAINS MALE FERTILITY AND TEMPERATURE-SENSITIVE PHENOTYPE.
PTM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES IN THE RS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ->S: IN TS2, TEMPERATURE-SENSITIVE
               DOMAIN (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERTILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHENOTYPE
                                                                                                                                                                                                                                                                                                              PIR; A31638; A31638.
PIR; A35846; A35846.
PIR; S12003; S12003;
F!YBase; FBGD003742; tra2.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50102; RRM, 1.
PROSITE; PS00030; RRM_RNP_1; 1.
                                                                                                                                                                                             EMBL; M23633; AAA28953.1; -. EMBL; X57484; CAA40722.1; -.
                                                                                                                                                                                                                                                                                   M76381; AAA69686.1; -.
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AAA28956.1
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MISSING: IN D3; GREATLY.REDUCED FEMALE-

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Gaps
SPECIFIC DSX SPLICING, RETAINS MALE
                                                           ö
                                      Length 264;
                                                           Indels
                  3BECBD694B0817B3 CRC64;
                                       DB 1;
                                      Score 43; DB 1
Pred. No. 6.9;
2; Mismatches
          FERTILITY
                   264 AA; 31031 MW;
                                      40.2%;
                           Query Match
Best Local Similarity 61...
Best Conservative
                                                                             6 TRTSGHLSRRSDH 18
                                                                                                30 TISSGHKDRRSDY 42
                   SEQUENCE
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Search completed: July 15, 2003, 16:30:29 Job time : 24 secs

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OM protein - protein search, using sw model

July 15, 2003, 16:30:06; Search time 78 Seconds (without alignments) 55.474 Million cell updates/sec Run on:

SEQ55-247-68

1 DRSNLTRTSGHLSRRSDHLSR 21

Title: Perfect scoré: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp_fungi:*
sp_human:*
sp_lnvertebrate:*
sp_mammal:* sp_archea:* sp_bacteria:* SPTREMBL_21:*

sp_organelle:* sp_phage:* sp_mhc:*

sp_v1rus:*
sp_vertebrate:* sp_plant:* sp_rodent:*

sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

					SUMMAKIES	
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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
+	ח	7.	'n	CT	Cyrabo	Naeabu sımıan t-IV
7	54	50.5	39	15	090NL6	Ogan16 simian t-lv
m	54	50.5	87	15	080794	
4	54	50.5	87	15	09PXZ8	
5	54	50.5	87	15	09PXY6	human
9	54	50.5	240	15	62X460	O9pxz9 human t-1vm
7	54	50.5	241		Q9PXY7	O9pxy7 human t-1vm
ω	53	49.5	532	S	Q9VC95	09vc95 drosophila
6	53	49.5	1765	2	Q8SX63	Q8sx63 drosophila
10	49	45.8	39	15	082210	082210 human t-1vm
11	47	43.9	65	15	012385	012385 simian t-ly
12	47	43.9	636	n	Q9Y8A4	Q9y8a4 aspergillus
13	46	43.0	96	7	Q54547	054547 streptococc
14	46	43.0	205	4	Q9Y4U5	09y4u5 homo sapien
15	46	43.0	416	16	Q8XZC3	Oêxzc3 ralstonia s
16	46	43.0	966	S	Q95XN3	Q95xn3 caenorhabdi

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Gaps

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Indels

51.4%; Score 55; DB 15; Length 39; 57.9%; Pred. No. 0.07;

2; Mismatches

Local Similarity 57.9 Les 11; Conservative

1 DRSNLTRTSGHLSRRSDHL 19

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Q9QNL6 PRELIMINARY; PRT; 39 AA. Q9QNL6; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

RESULT 2 Q9QNL6 ID Q9QN AC Q9QN DT 01-M

NON_TER SEQUENCE Query Match Best Loca Matches

	m	fremyella	Q9JSX4 neisseria m	loichmania	- (>	095ul7 drosophila	09hrq1 halobacteri	O9vlh3 drosophila	Q80353 human immun	Q70111 human immun	Q9v734 drosophila	090x53 xenopus lae	U933tZ numan 1mmun	Q9aU1U streptococc	QSHQI/ SCIONGYIOCE Oggici salmonella	Ogolh7 homo sapien	O9bwh8 homo sapien	Q9hr09 halobacteri			drosophila	neisseria		Uysiss arabidopsis	Oovres arabicopsis Oglul4 arabicopsis	ALIGNMENTS			39 AA.		sequence update)	annotation update)			Similan i lympholiopic viius 1. Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.				. T	Ξ).";	the EMBL/Genbank/DDBJ databases.			22DC9D56743F139F CRC64;
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MEDIINE-88232270; PubMed-2897612;
Tsujimoto A., Teruuchi T., Imamura J., Shimotohno K., Miyoshi I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence analysis of a provirus derived from HTLV-1-associated myelopathy (HAM).";
MAI. B101. Med 5:29-4(1988).
EMBL. M373011. AA445391.1; -.
SEQUENCE 87 AA, 9963 MW; 141F3B7BAB33BB273 CRC64;
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                                                                            STRAIN-CH-REGINA;
Niphuis H., Verschoor E.J., Heeney J.L.;
Reduced transmission and prevalence of HTLV-1/STLVcpz by breeding of chimpanzees (Pan troglodytes).";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; Y18904; CAB52548.1; -
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Pred. No. 0.23;
2; Mismatches 2; Indels
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                      Simian T-lymphotropic virus 1.
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
NCBI_TaxID=33747;
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Human T-lymphotropic virus 1.
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
NCBI_TaxID=11908;
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Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
NCBI_TaxID=11908;
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 (TrEMBLrel. 21, Last annotation update)
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Gessain A., Boeri E., Yanagihara R., Gallo R.C., Franchini G.;
"Complete nucledide sequence of a highly divergent human T-cell
leukemia (lymphotropic) virus type I (HTLV-I) variant from melanesia:
genetic and phylogenetic relationship to HTLV-I strains from other
geographical regions.";
J. Virol. 67:1015-1023(1993)
SEQUENCE 87 AA; 9988 MW; 34A239AC7EE7D9CD CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 89:8813-8817(1992),
SEQUENCE 87 AA: 10080 MW; 12DDEDBDE6838B277 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
p30 II protein.
Human T-lymphotropic virus 1.
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
NCBI_TaxID=11908;
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Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
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Q85X63 Best Loca Matches Matches RAHRAH RA δλ g ã g RAY MEDELINE-2019606; PubMed=10731132;
RAY Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Admantides P.G., Scherer S.E., Li P.W., Hooksins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J. Evangelista C.C., Ferraz C., Ferricra S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferricra S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wen H.-H., Ibegwam C.,
Alalii M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A., ö Drosophila melanogaster (Fruit fly). Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Koralnik I.J., Gessain A., Klotman M.E., Lo Monico A., Berneman Z.N., Gaps ö Score 54; DB 15; Length 241; Pred. No. 0.67; Franchini G.;
"Protein isoforms encoded by the pX region of human T-cell leukemia/lymphotropic virus type I.";
Proc. Natl. Acad. Sci. U.S.A. 89:8813-8817(1992).
SEQUENCE 241 AA; 26791 MW; 7607FIF66C55CF5E CRC64; 2; Indels PX-TAX-ORF II fusion protein.
Human T-Lymphotropic virus 1.
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus
NCBI_TaxID=11908; O9PXY7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Liu X., Martei B., McIntosh T.C., McLeod M.P., McDherson D., A. Merkulov G., Milshina N.V., McDeod M.P., McDherson D., McArtulov G., Milshina N.V., McDarry C., Morris J., Moshrefi A., A. Merkulov G., Milshina N.V., Misohry C., Morris J., Moshrefi A., A. Mount S.M., Moy M., Murphy B., Murphy L., Muskern D.R., Pacled J.M., Ralazolo M., Pittman GS., Fan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., A. Spier E., Siden Kiamos I., Simpson M., Skrupski M.P., Smith T., Shor B.C., Stapletcon M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassamman D.A., Weinsteck G.M., Weissenbach J., R. Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q. A., R. W. J., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O., R. The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

R. Science 2831:185-2195(2000). Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Gaps Gaps Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., ; 49.5%; Score 53; DB 5; Length 1765; 58.8%; Pred. No. 7.7; 49.5%; Score 53; DB 5; Length 532; 58.8%; Pred. No. 2.2; 5; Indels EMBL; AY094828; AAM11181.1; -. SEQUENCE 1765 AA; 195942 MW; 6AF1A6933FA482C3 CRC64; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. 532 AA; 58615 MW; F2A7D2861E1F3469 CRC64; (TrEMBLrel. 21, Created) (TrEMBLrel. 21, Last sequence update) (TrEMBLrel. 21, Last annotation update) PRT; 1765 AA 2; Mismatches 2; Mismatches PRINTS; PR00503; BROWDODARIN.
PRINTS; PR01574; TUBBYPROTEIN.
SMART; SM00297; BROMO; 1.
PROSITE; PS50014; BROMODMAIN_2; 1.
SEQUENCE 532 AA; 58615 MF. FlyBase; FBgn0039181; CG6400. InterPro; IPR001487; Bromodomain. 1:| |||| || :|| 1299 RANGTRISSHLGAENDH 1315 380 RANGIRISSHLGAENDH 396 Pfam; PF00439; bromodomain; 1. 2 RSNLTRTSGHLSRRSDH 18 2 RSNLTRTSGHLSRRSDH 18 10; Conservative Local Similario, hes 10; Conservative PRELIMINARY; Best Local Similarity SEQUENCE FROM N.A. STRAIN-BERKELEY; 01-JUN-2002 (01-JUN-2002 (01-JUN-2002 (Query Match Query Match

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Elrod S.L., Jones A., Cherry J.R.; "Cloning of 5-aminolevulinate synthase from Aspergillus oryzae and its use as a selectable marker.";
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STRAIN-M TYPE 30;
MEDLINE-95198537; PubMed-7891551;
Whatmore A.M., Kapur V., Sullivan D.J., Musser J.M., Kehoe M.A.;
Whotmore A.M., Rapur V., Sullivan D.J., Musser J.M., Kehoe M.A.;
"Non-congruent relationships between variation in emm gene sequences and the population genetic structure of group A streptococci.";
MMO1. Microbiol. 14:619-631(1994).

EMBL. Ull944; AAA99560.1; -.
                                                                                                   Aspergillus oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Streptococcaceae; Streptococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hesis (1993), Microbiology, University of Newcastle Upon Tyne.
                                                                                                                                                                                                                                                                                                                                              Submitted (Max-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF152374; AAD38391.1; -
InterPro; IPR001408; Ala_synthase.
InterPro; IPR001917; Maniotransf1/2.
InterPro; IPR001917; MHransf_2.
Pfam; PF02490; ALA_synthase; 1.
Pfam; PF00155; aminotran1_2; 1.
PROSITE; PS00599; AA_TRANSFER_CIASS_2; 1.
SEQUENCE 636 AA; 68145 MW; F70BC2A073A0CDBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 96
96 AA; 10640 MW; E6A9BC38FFB4B865 CRC64;
                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.9%; Score 47; DB 3;
42.1%; Pred. No. 26;
iive 3; Mismatches
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Pred. No. 5.3;
6; Mismatches
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                                                                                  5-aminolevulinic acid synthase
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 38.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                     STRAIN-A1560;
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Yanaghara R., Saitou N., Nerurkar V.R., Song K.J., Bastian I.,
Yanaghara R., Gajdusek D.C.;
"Molecular phylogeny and dissemination of human T-cell lymphotropic
"Molecular phylogeny and dissemination of primate evolution and human migration.";
wirus type I viewed within the context of primate evolution and human migration.";
Cell. Mol. Biol. 0:0-0(1995).
EMBL: Ul2121; AAA99642.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of a simian T-lymphotropic virus from a wild-caught orangutan (Pongo pygmaeus) from Kalimantan, Indonesia."; J. Gen. Virol. 79:51-55(1998).
EMBL: Y13146; CAA73607.1; -.
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Pred. No. 0.67;
2; Mismatches 3; Indels
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Pred. No. 2.4;
2; Mismatches 3; Indels
                                                                                                                                                                                                        Human T-lymphotropic virus 1.
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
NCBI_TaxID=11908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simian T-lymphotropic virus 1.
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
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                                                                                                       (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Rex p13/p30 protein (Fragment).
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Best Local Similarity 64.3%;
Matches 9; Conservative
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23 SRPTGHLPRTSDHL 36
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24 SRPTGHLSRASGHL 37
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9; Conservative
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01-NOV-1996 (
01-JUN-2002 (
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Q9Y8A4
ID Q9Y8A4
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              RESULT 10
Q82210
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7 RTSGHLSRRSDHLSR 21 | :||::| || | 312 RLAGHIARWSDHAQR 326

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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"Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
                                                                                                                         Homo sapiems (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TIEMBLIEL. 20, Created)
01-MAR-2002 (TIEMBLIEL. 20, Last sequence update)
01-WAR-2002 (TIEMBLIEL. 21, Last annotation update)
Probable 8-amino-7-oxonomanoate synthase protein (EC 2.3.1.47).
BIOF OR RSC1478 OR RS03827.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria: Proteobacteria; beta subdivision; Ralstonia group;
Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.0%; Score 46; DB 16; Length 416; 53.3%; Pred. No. 24; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 4; Length 205;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Program PF00490; ALA synthase; 1.
Pfam: PF00155; aminotran_1_2; 1.
Transferase; Acyltransferase; Complete proteome.
SEQUENCE 416 AA; 43676 MW; 1CED02079365489F CRC64;
                                                                                                                                                                                                                                                                                                                                205 AA; 21548 MW; D88EB7A823C618E4 CRC64;
                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NFPOThetical 21.5 kDa protein (Fragment).
                             205 AA
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InterPro; IPR003408; Ala_synthase.
InterPro; IPR004839; Aminotransf1/2.
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                               PRT;
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MEDLINE=21681879; PubMed=11823852;
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Best Local Similarity 69.2
Matches 9; Conservative
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Best Local Similarity 53,3
Matches 8; Conservative
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                               PRELIMINARY;
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                                               09Y4U5;
                               Q9Y4U5
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RESULT 14
Q9Y4U5
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OM protein - protein search, using sw model

Run on:

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23.765 Million cell updates/sec July 15, 2003, 16:30:01; Search time 26 Seconds

Perfect score:

SEQ55-247-68 107 1 DRSNLTRTSGHLSRRSDHLSR 21 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

262574 segs, 29422922 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA: Database

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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

4	Describtion	Sequence 97, Appl	18,	94,	96	2,2	7	7	2,	7	95,	11,	16,	16,	22,	22,	Sequence 12, Appl	2, 4	σ	311	Sequence 49, Appl	Sequence 50, Appl	4, 2	4	ω,	e,	48,	7, 1
£.		US-09-229-007A-97	US-07-743-518-18	US-09-229-007A-94	US-09-229-007A-96	US-08-871-266B-2	US-08-819-458A-2	US-09-018-864A-2	-08-871-	US-09-618-419-2		US-08-856-841-11	-08-871-	1	US-08-871-267B-22	-03	US-08-961-083-12	US-09-147-522-2	US-09-229-007A-93	US-09-134-001C-3116	٠	-09-042	-621-	US-08-945-567D-4	US-08-621-944A-3	US-08-945-567D-3	-268-	US-09-068-655-7
2	9 :	4	7	4	4	~	7	7	ო	4	4	4	7	7	m	4	4	ო	4	4	m	m	4	4	4	4	4	4
- 4500 T	neng cm	21	40	21	21	636	636	636	636	636	21	169	649	649	649	649	312	478	21	484	1050	1050	1833	1833	1992	1992	2048	218
& Query Match		54.2	50.5	49.5	47.7	43.9	43.9	43.9	•	43.9	43.0	39.3	39.3	39.3	39.3	39.3	38.3	38.3	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	36.4
9	2000	28	54	53	51	47	47	47	47	47	46	42	42	42	42	42	41	41	40	40	40	40	40	40	40	40	40	39
Result		1	7	3	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

,,,	Sequence 1, Appli Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 51, Appl	Sequence 4, Appli	Sequence 7, Appli	Sequence 26, Appl	Sequence 26, Appl	Sequence 175, App							
US-08-303-238-1	US-U8-438-834-1 US-08-843-521-2	US-09-012-871-2	US-08-981-690-2	US-07-872-644-51	US-08-297-494-51	US-08-297-510-51	US-08-479-532-51	US-08-455-526-51	US-08-455-525-51	US-09-139-491-51	PCT-US92-03222-51	US-08-448-170-4	US-08-961-803-7	US-08-938-830-26	US-09-020-222-26	US-08-711-417C-175
П.	* ←	4	N	Н	Н	П	٦	П	Ч	٣	Ŋ	Н	4	r	m	4
376	783	783	260	634	634	634	634	634	634	634	634	725	725	907	907	236
36.4	36.4	36.4	36.0	35,5	35.5	35.5	35.5	35.5	35.5	35.5	35.5	35.5	35.5	35.0	35.0	34.6
39	n 60	39	38.5	38	38	38	38	38	38	38	38	38	38	37.5	37.5	37
78	30	31	32	33	34	35	36	37	38	38	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Jamieson, Andrew
APPLICANT: Jamieson, Andrew
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Forcients and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: to Bind to Preselected Sites
FILE REFERENCE: 019496-001800US
CURRENT APPLICATION NUMBER: US/09/229,007A
UNDBER OF SEQ ID NOS: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ). OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence; CTBER INFORMATION: (F1, F2, F3) from SBS design GL-8.3.1 US-09-229-007A-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MILLER, MARK
APPLICANT: GARRUTO, RALPH M.
TITLE OF INVENTION: PAPUR NEW GUINEA HUMAN T-LYMPHOTROPIC
TITLE OF INVENTION: VIRUS
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 54.2%; Score 58; DB 4; Length 21; Best Local Similarity 55.0%; Pred. No. 0.0025; Matches 11; Conservative 5; Mismatches 4; Indels
US-09-229-007A-97; Sequence 97, Application US/09229007A; Patent No. 6453242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/07743518
Patent No. 5397696
GENERAL INFORMATION:
APPLICANT: YANAGIHARA, RICHARD
APPLICANT: NERURKAR, VIVEK R.
APPLICANT: JENKINS, CAROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RSNLTRTSGHLSRRSDHLSR 21
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                                                                                                                               Case, Casey C.
Cox III, George N.
Jamieson, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 97
LENGTH: 21
TYPE: PRT
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US-07-743-518-18
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No. 58719910 No. 5871991disk Of No. 5871991th America, Inc.
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APPLICANT: Elrod, Susan L.
APPLICANT: Cherry, Joel R.
TITLE OF INVENTION: Aspergillus Oryzae 5-Aminolevulinic
TITLE OF INVENTION: Acid Synthases And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 Lexington Avenue - 64th Fl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/871,266B
                                                                                                                                                     Sequence 96, Application US/09229007A Patent No. 6453242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08871266B Patent No. 5871991
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SNLTRISGHLSRRSDHLSR 21
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REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER:
                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.9%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                  US-09-229-007A-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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APPLICANT: Case, Casey C.
APPLICANT: Case II, George N.
APPLICANT: Banisson, Andrew
APPLICANT: Rebar, Edward:
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: 1996-001080005
CURRENT APPLICATION NUMBER: US/09/229,007A
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,518
FILING DATE: 19910812
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                          WTS/5683/84699/SAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 1;
Pred. No. 0.024;
2; Mismatches
                      DARBY & CUSHMAN
                                                                                                       COUNTRY: U.S.A.
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 94, Application US/09229007A Patent No. 6453242
                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION UNDBER: 26,581
REFERENCE/DOCKET NUMBER: WFS/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-300
TELEFAX: 202-861-300
TELEFAX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                         1615 L STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Eisenberg, Stephen P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 71.4
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-07-743-518-18
CORRESPONDENCE ADDRESS:
                                         STREET: 1615 L ST
CITY: WASHINGTON
STATE: D.C.
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                      ADDRESSEE:
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of Designing Zinc Finger Proteins
                                                                                                                                                                                                                                                                           APPLICANT: Eisenberg, Stephen P.
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Case, Casey C.
APPLICANT: Case, Casey C.
APPLICANT: Case II, George N.
APPLICANT: Jamieson, Andrew
APPLICANT: Sangamo Bioschences, Inc.
ITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
ITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Prote
ITLE OF INVENTION: De Bind to Preselected Sites
ITLE OF INVENTION: LO Bind to Preselected Sites
CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEC ID NO 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence; OTHER INFORMATION: (F1, F2, F3) from SP1
US-09-229-007A-96
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Pred. No. 0.035;
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TELEPHONE:

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CITY: New York
                                                                                                                                                                                                                                                                                 USA
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-371-267B-2
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                                                                                                                                                                                                                                              CITY:
STATE:
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STREET: 405 Lexington Avenue
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jensen, Ejner B.
APPLICANT: Cherry, Joel
APPLICANT: Elrod, Susan L.
TITLE OF INVENTION: Methods For Producing Polypeptides
TITLE OF INVENTION: In Respiratory-Deficient Cells
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFRWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,458A
                                                                                                                                                                                                        ; Score 47; DB;
; Pred. No. 8.3;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB;
Pred. No. 8.3;
3; Mismatches
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531 ERLRITPTPGHIKEHRDHL 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 17-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/TOCKET NUMBER: 5115
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-667-0123
                                                                                                                                                                                                                                                                             1 DRSNLTRTSGHLSRRSDHL 19
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Best Local Similarity 42.1%;
Matches 8; Conservative
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Best Local Similarity 42.1%;
Matches 8; Conservative
                             INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 636 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 636 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 212-878-9655
                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58916
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61000570 No. 6100057disk Of No. 6100057th America, Inc.
STREET: 405 Lexington Avenue - 64th Fl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                        APPLICANT: Elrod. Susan L.
APPLICANT: Elrod. Susan L.
APPLICANT: Cherry, Joel R.
TITLE OF INVENTION: Aspergillus Oryzae 5-Aminolevulinic
TITLE OF INVENTION: Acid Synthases And Nucleic Acids. Encoding Same
TUTBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59587470 No. 5958747disk Of No. 5958747th America,
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Patent No. 6100057
GENERAL INFORMATION:
APPLICANT: Cherry, Joel R.
APPLICANT: Cherry, Joel R.
APPLICANT: Jones, Aubrey
ATILE OF INVENTION: Production in Filamentous Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 2;
Pred. No. 8.3;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA: US/09/018 07:15 FILING DAME: US/09/018 07:15
Sequence 2, Application US/09018864A Patent No. 5958747 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/871,266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        531 ERLRITPTPGHIKEHRDHL 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-9652
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.98;
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 636 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 amino ació
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                          Diskette
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internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                    ZIP: 10174
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
Matches 8; Conserv
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APPLICANT: Case, Casey C.
APPLICANT: Case, Casey C.
APPLICANT: Cox III. George N.
APPLICANT: Standard J.
APPLICANT: Sangamo Bloaslences, Inc.
APPLICANT: Sangamo Bloaslences, Inc.
APPLICANT: Sangamo Bloaslences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: to Bind to Preselected Sites
CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1999-01-12
SUFFRAME: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence; OTHER INFORMATION: (F1, F2 and F3) from Zif 268
US-09-229-007A-95
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TITLE OF INVENTION: OR POLYPEPTIDES FROM THE PARVOVIRUS B19
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                                               Length 636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 43.0%; Score 46; DB 4; Length 21; Best Local Similarity 58.8%; Pred. No. 0.23; Matches 10; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                               DB 4;
8.3;
                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-618-419-2
                                                                                                                                                                                                                                                                                               Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 95, Application US/09229007A Patent No. 6453242
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Sequence 11, Application US/08856841
Patent No. 6274307
GENERAL INFORMATION:
APPLICANT: ERWIN SOUTSCHEK
APPLICANT: MANFRED MOTZ
TELEFAX: 212-878-9655
TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  :| :| || || 531 ERLRITPTPGHIKEHRDHL 549
                                                                                                                                                                                                                                                                                                                                                                                        1 DRSNLTRTSGHLSRRSDHL 19
                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Elsenberg, Stephen P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LTRTSGHLSRRSDHLSR 21
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                                                                                                                                                                                                                                                                                               43.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.13
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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ADDRESSEE: No. 62618270 No. 6261827d1sk Of No. 6261827th America, Inc. STREET: 405 Lexington Avenue - 64th Fl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5EO for Windows Version 2.0
CURRENT APPLICATION DATA:
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FILING DATE: 18-Jul-2000
PRIOR APPLICATION NUMBER: 08/871,267
APPLICATION NUMBER: 08/871,267
FILING DATE: 9-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, Carol E.
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 4771.200-US
TELECOMMUNICATION INFORMATION:
                                                                                                  CURRENT SYSTEM: DOS SOFTWARE: FastEEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/871,267B FILING DATE: 9-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 43.9%; Score 47; DB Best Local Similarity 42.1%; Pred. No. 8.3 Matches 8; Conservative 3; Mismatches
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531 ERLRITPTPGHIKEHRDHL 549
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Patent No. 6261827
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                                                                                                                                                                                                                                                                                             36,993
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-9652
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APPLICANT: Elrod, Susan L.
Cherry, Joel R.
Jones, Aubrey
                                                                                      IBM Compatible
                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, CAIOL E.
REGISTRATION NUMBER: 36,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 39
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 636 amino acida TYPE: amino acid
                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: protein
IS-08-871-2678-2
                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
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                10174
                                                                                           COMPUTER:
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FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: SERUM FROM PATIENT WITH ACUTE
ORIGINAL SOURCE: INFECTION (ERYTHEMA INFECTIOSUM)
IMMEDIATE SOURCE: GENETICALLY ENGINEERED PEPTIDE
POSITION IN GENOME: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE: PARVOVIRUS-LIKE PARTICLES IN HUMAN SERA
JOURNAL: LANCET
VOLUME: I
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                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/214,658
FILING DATE: 16-MARCH-1994
APPLICATION NUMBER: US 07/917,096
FILING DATE: 4-AUGUST-1992
APPLICATION NUMBER: PCT/DE91/00106
FILING DATE: 8-FEBRUARY-1991
APPLICATION NUMBER: DE40038262
FILING DATE: 8-FEBRUARY-1990
ATTONNEY, AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REGISTRATION NUMBER: 27,224
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAUX: (212) 697-3355
                                                                                                    MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
                                                                                                                                                                 SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,841
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
PUBLICATION INFORMATION:
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AUTHORS: FRITSCH, E.F.
AUTHORS: SAMBROOK, J.
TITLE: MOLECULAR CLONING
JOURNAL: COLD SPRING HARBOR, NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11:
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AUTHORS: COSSART, Y.E.
AUTHORS: FIELD, A.M.
AUTHORS: MIDDOWS, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION: PEPTIDE POTHETICAL: N/A
                                                                                  COMPUTER READABLE FORM:
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NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N/A
                                      USA
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                                          COUNTRY:
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SSEE: NO. 58719910 No. 5871991disk Of No. 5871991th America, Inc. 1405 Lexington Avenue - 64th Fl. New York
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US-08-871-266B-16
Sequence 16, Application US/08671266B
Patent No. 5871991
GENERAL INFORMATION:
APPLICANT: Elrod, Susan L.
APPLICANT: Cherry, Joel R.
TITLE OF INVENTION: Aspergillus Oryzae 5-Aminolevulinic
TITLE OF INVENTION: Acid Synthases And Nucleic Acids Encoding Same NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              39.3%; Score 42; DB 4; Length 169; 66.7%; Pred. No. 12; Live 2; Mismatches 2; Indels
                                                                                                                SINGLE STEP PURIFICATION OF POLYPEPTIDES SINGLE SIPERSESIN ESCHERICHIA COLI AS FUSIONS WITH GLUTATHIONE S. TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,266B
              FILING DATE:
PUBLICATION DATE:
RELEAVAT RESIDUES IN SEQ ID NO: 11:
PUBLICATION INFORMATION:
AUTHORS: SMITH, D.B.
                                                                                                                                                                                                                                                                                                     DOCUMENT NUMBER:
FILLING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER:
TELECHONE: 212-878-9652
TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 649 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
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| GILSRRPDHMSK 12
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Best Local Similarity
Matches 8; Conserv
DOCUMENT NUMBER:
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                                                                                                                                                                                TITLE: GI
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                          US-08-856-841-11
                                                                                                                    AUTHORS:
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                                                                                                                                            TITLE:
TITLE:
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MOLECULE TYPE:

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linear
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                             COUNTRY:
                                                                                                                                           STATE:
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                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Elrod, Susan L.
APPLICANT: Cherry, Joel R.
TITLE OF INVENTION: Aspergillus Oryzae 5-Aminolevulinic
TITLE OF INVENTION: Acid Synthases And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59587470 No. 5958747th America, Inc.
STREET: 405 Lexington Avenue - 64th Fl.
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                    Length 649;
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                                    DB 2;
56;
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56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATIS: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,864A
                                    Score 42; DB Pred. No. 56; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/08871267B Patent No. 6100057 GENERAL INFORMATION:
APPLICANT: Elrod, Susan L. APPLICANT: Cherry, Joel R.
                                                                                                                                                                                                                          Sequence 16, Application US/09018864A
Patent No. 5958747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/871,266
                                                                                                                            :| :| || || 551
533 ERLRITPIPGHTQELRDHL 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTOREY AGENT.
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-9652
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| :| | || 533 ERLRITPTPGHTQELRDHL 551
                                                                                                     1 DRSNLTRTSGHLSRRSDHL 19
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                                Query Match 39.3%;
Best Local Similarity 42.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: NO. 5958747e
US-09-018-864A-16
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ilarity 42.1%;
Conservative
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LENGTH: 649 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 8; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
US-08-871-266B-16
                                                                                                                                                                                                        US-09-018-864A-16
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ADDRESSEE: No. 62618270 No. 6261827disk Of No. 6261827th America, Inc. STREET: 405 Lexington Avenue - 64th Fl.
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                                                              ADDRESSEE: No. 61000570 No. 6100057disk Of No. 6100057th America, Inc. STREET: 405 Lexington Avenue - 64th Fl.
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Patent No. 6261827
GENERAL INFORMATION:
GENERAL INFORMATION:
Cherry, Joel R.
Jones, Aubrey, Amethod for Increasing Hemoprotein
Production in Filamentous Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 649;
TITLE OF INVENTION: A Method for Increasing Hemoprotein TITLE OF INVENTION: Production in Filamentous Fungi NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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ComporER: 1BM Compatible
OPERATING SYSTEM: DS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                          COMPUTER REACABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER REACABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,267B
FILING DATE: 9-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROZGK, CATOL E.
REGISTRATION NUMBER: 36,993
REFERRUGE/DOCKET NUMBER: 4771.200-US
TELEPHONE: 212-878-9552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.3%; Score 42; DB 3; llarity 42.1%; Pred. No. 56; Conservative 2; Mismatches
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APPLICATION NUMBER: US/09/618,419
FILING DATE: 18-Jul-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DRSNLTRTSGHLSRRSDHL 19
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US-08-871-267B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA ZIP: 10174 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 649 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCES: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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OM protein - protein search, using sw model

July 15, 2003, 16:30:36; Search time 21 Seconds (without alignments) 116.420 Million cell updates/sec Run on:

SEQ55-247-68 107 Title: Perfect score:

1 DRSNLTRTSGHLSRRSDHLSR 21 Sequence:

BLOSUM62 Gapext 0.5 Scoring table:

445758 seqs, 116419773 residues Searched:

445758 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published_Applications_AA:*

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/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Sequence 97, Appl		Sequence 96, Appl	95,	9999	Sequence 5, Appli	Sequence 11688,	Sequence 7810, Ap	Sequence 635, App			Sequence 12, App	Sequence 4, Appli	Sequence 196, App	Sequence 196, App	196,	Sequence 196, App	Sequence 196, App	196,
COMMUNICA	ΩI	US-10-113-424-97	US-10-113-424-94	US-10-113-424-96	US-10-113-424-95	US-09-738-626-6666	US-10-071-894-5	0 US-09-815-242-11688	US-10-156-761-7810	US-10-091-504-635	0 US-09-908-711-69	0 US-09-764-869-635	0 US-09-765-272-12	US-09-769-787-4	US-10-028-072-196	US-10-121-049-196	US-10-123-904-196	US-10-140-470-196	US-10-175-746-196	US-10-176-918-196
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dP	Query	54.2	49.5	47.7	43.0	42.1	41.6	40.2	39.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3
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	Result No.	1	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19

RESULT 2 US-10-113-424-94 Sequence 94, Application US/10113424

2 RSNLTRTSGHLSRRSDHLSR 21 ::| || || ||: ||||:||:|| 2 KDSLVRTSDHLASRSDNLFR 21

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US-10-176-921-196 Sequence 196, App US-10-137-865-196 Sequence 196, App Sequence 196, App US-10-140-474-196 Sequence 196, App US-10-143-114-196 Sequence 196, App US-10-143-114-196 Sequence 196, App US-10-123-262-196 Sequence 196, App US-10-123-262-196 Sequence 196, App US-10-123-262-196 Sequence 196, App US-10-141-755-196 Sequence 196, App US-10-141-755-196 Sequence 196, App US-10-123-261-196 Sequence 196, App US-10-123-261-196 Sequence 196, App US-10-123-261-196 Sequence 196, App US-10-123-261-196 Sequence 196, App US-10-123-291-196 Sequence 196, App US-10-123-292-196 Sequence 196, App US-10-123-291-196 Sequence 196, App US-10-123-292-196 Sequence 196, App US-10-123-293-196 Sequence 196, App US-10-123-294 Sequence 196, App US-10-123-294 Sequence 196, App US-10-123-294 Sequence 196, App US-10-123-294 Sequence 1	ALIGNMENTS 10-113-424-97 equence 97, Application US/10113424 equence 97, Application US/10113424 equence 97, Application US/10113424 equence 97, Application US/10113424 equence 97, Application US/2030105593A1 APPLICANT: Eisenberg, Stephen P. APPLICANT: Case, Casey C. APPLICANT: Edward J. APPLICANT: Amieson, Andrew APPLICANT: Amieson, Andrew APPLICANT: Amieson, Andrew APPLICANT: Sangamo Biosciences, Inc. TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger TITLE OF INVENTION: to Bind to Preselected Sites CURRENT APPLICATION NUMBER: US/09/229,007A PRIOR FILING DATE: 1999-01-12 NUMBER OF SEQ ID NOS: 97 EDWATH: 21 TYPE: PRESENTE: PatentIn Ver. 2.1 EDWATH: 21 TYPE: PRESENTE: PATENTICIAL Sequence FEATURE: OFFERE INFORMATION: Description of Artificial Sequence: ZFP Sequence OTHER INFORMATION: (F1, F2, F3) from SBS design GL-8.3.1	Score 58; DB 9; Length 21; Pred. No. 0.0088; 5; Mismatches 4; Indels 0; Gaps 0;
00000000000000000000000000000000000000	SULT 1 Sequence 97, Application US/1011342 Publication No. US20030105593A1 GENERAL INPORMATION: APPLICANT: Eisenberg, Stephen P. APPLICANT: Case, Casey C. APPLICANT: Cox III, George N. APPLICANT: Rebar, Edward J. APPLICANT: APPLICATION NUMBER: US/10/22 NUMBER OF SEQ ID NOS: 97 LENGTH: LANG DATE: 1999-01-12 TYEE: PAT TYEE PRT TYEE TYEE PRT TYEE TYEE TYEE TYEE TYEE TYEE TYE	54.2%; larity 55.0%; Conservative
	424-97 15. 97, Application Universely 100 No. US200301055 16. 10. No. US200301055 18. 15. 15. 15. 16. 16. 16. 16. 16. 16. 16. 16. 16. 16	겉
4444444444444444444	SULT 1 Sequence 97, Applic Publication No USZ GENERAL INFORMATION APPLICANT: Elsenbe APPLICANT: Case, of APPLICANT: Sangum TITLE OF INVENTION FILE REPERENCE: 01 CURRENT APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION PRIOR APPLICATION CURRENT FILING DATE PRIOR FILING DATE PRIOR FILING DATE PRIOR FILING DATE PRIOR FILING DATE CURRENT SEQ ID NO SEQ ID NO SEQ ID NO 97 LENGTH: 21 TYPE: PRT ORGANISM: ALLIFIC PEATURE: ORGANISM: ALLIFIC FEATURE: OTHER INFORMATION CTHER INFORMATION-10-113-424-97	Match Local Sines Les 11;
01222222222222222222222222222222222222	RESULT 1 US-10-113-42 Sequence 9 Publicatio GENERAL IN APPLICANT APPLICANT APPLICANT APPLICANT TITLE OF TITLE OF TITLE REFE CURRENT F FILE REFE CURRENT F FILE REFE CURRENT F FILE REFE CURRENT F TITLE REFE CURRENT F CURREN	Query Match Best Local Matches 1

Publication No. US20030105593A1

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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6666, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Corynebacterium glutamicum
US-09-738-626-6666
                                      Sequence 95, Application US/10113424
Publication No. US20030105593A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LTRTSGHLSRRSDHLSR 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NOS:
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LENGTH: 1610
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SOFTWARE:
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APPLICANT: Case, Case, Casey C.
APPLICANT: Jamieson, Andrew
APPLICANT: Jamieson, Andrew
APPLICANT: Sangamo Blosciences, Inc.
APPLICANTION: Proteins and Methods of Designing 2inc Finger Proteins
TITLE OF INVENTION: to Bind to Preselected Sites
TITLE OF INVENTION: to Bind to Preselected Sites
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US/09/229,007A
PRIOR APPLICATION NUMBER: US/09/229,007A
PRIOR APPLICATION NUMBER: US/09/229,007A
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                      Designing Zinc Finger Proteins
            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence ; OTHER INFORMATION: (F1, F2 and F3) from SBS design GR-223 US-10-113-424-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COTHER INFORMATION: Description of Artificial Sequence: ZFP sequence; OTHER INFORMATION: (F1, F2, F3) from SP1
US-10-113-424-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 96, Application US/10113424 Publication No. US20030105593A1 GENERAL INFORMATION:
APPLICANT: Eisenberg, Stephen P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SNLTRISGHLSRRSDHLSR 21
APPLICANT: Eisenberg, Stephen P. APPLICANT: Case, Casey C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SNLTRTSGHLSRRSDHL 19
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                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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il Similarity 57.9%;
il; Conservative
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Best Local Similarity
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Matches 10; Conserv
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US-10-113-424-96
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APPLICANT: Elsenberg, Stephen P.
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Case, Casey C.
APPLICANT: Cox III, George N.
APPLICANT: Ox III, George N.
APPLICANT: Andrew
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
FILE REPRENCE: 019496-001800US
CURRENT APPLICATION NUMBER: US/J0/113,424
CURRENT FILING DATE: 2002-03-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 2FP sequence
OTHER INFORMATION: (F1, F2 and F3) from 21f 268
US-10-113-424-95
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43.0%; Score 46; DB 9;
Best Local Similarity 58.8%; Pred. No. 0.71;
Matches 10; Conservative 1; Mismatches
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRICR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/229,007A PRIOR FILING DATE: 1999-01-12 NUMBER OS SEQ ID NOS: 97 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 95
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Gaps

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Sequence 635, Application US/10091504
; Publication No. US20030059908A1
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C1
; CURRENT FALLIGATION NUMBER: US/10/091,504
; CURRENT FILIG DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 635
; LENGTH: 140
                                                                                                                                                                          DB 10; Length 105;
13;
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46.7%; Pred. No. 1.5e+02;
tive 5; Mismatches 3.
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Pred. No. 13;
4; Mismatches
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APPLICANT: SARAKI, VOSHIVUKI.
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFRENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7810
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11688
LENGTH: 105
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7810, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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                                                                                   TYPE: PRT
CRGANISM: Klebsiella pneumoniae
US-09-315-242-11688
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475 LTRINGNATRRNSHI 489
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Best Local Similarity 50.0%;
Matches 9; Conservative
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HORIKAWA, HIROSHI
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Best Local Similarity 46.7
Matches 7; Conservative
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US-10-156-761-7810
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US-10-091-504-635
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             42.1%; Score 45; DB 9; Length 1610;
42.9%; Pred. No. 1.4e+02;
Live 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                        APPLICANT: Lorenz, Michael C.
APPLICANT: Fink, Gerald R.
APPLICANT: Fink, Gerald R.
TITLE OF INVENTION: Glyoxylate Cycle Enzymes as Targets for TITLE OF INVENTION: Antifungal Drug Development
FILE REPERENCE: 0399.2026-001
CURRENT APPLICATION UNMERS: 105/10/071,894
PRIOR APPLICATION NUMBER: 60/267,622
PRIOR PLING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTESO for Windows Version 4.0
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.6%; Score 44.5; I
30.8%; Pred. No. 40;
tive 10; Mismatches
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/269,308
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                                                                                                        1 DRSNLTRTSGHLSRRSDHLSR 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                     Best Local Similarity 42.99
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: A. thaliana AceA US-10-071-894-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 30.8
Matches 8; Conservative
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                  Query Match
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APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REBERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 10; Length 140;
Pred. No. 38;
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Pred. No. 38;
1; Mismatches 4; Indels
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                     PRIOR APPLICATION UNDBER: USO1/01341
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: USO1/0136
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
SOFTWARE: PATENTING NUMBER: 60/209,467
PRIOR FILING DATE: 2000-06-07
SOFTWARE: PATENTING DATE: 2000-06-07
SOFTWARE: PATENTING DATE: 2000-06-07
PRIOR PRIOR PRIOR PATENTING NUMBER: 60/209,467
PRIOR PRIOR PATENTING DATE: 2000-06-07
PRIOR PRIOR PATENTING DATE: 2000-06-07
PRIOR PRIOR PATENTING NUMBER: 60/209,467
PRIOR PRIOR
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Best Local Similarity 64.3%;
Matches 9; Conservative
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Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRCANISM: Homo sapiens
US-09-908-711-69
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US-09-764-869-635
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LENGTH: 140
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Sequence 69, Application US/09908711

Sequence 1 WOORMATON:

SEQUENCE INVERTION:

TILL OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA128

CURRENT APPLICATION NUMBER: US/09/908,711

CURRENT FILING DATE: 2001-07-20

PRIOR FILING DATE: 2001-01-17

PRIOR SPELICATION NUMBER: US/09/908,711

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: US/04,867

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17
                                       4; Indels
64.3%; Pred. No. 38;
tive 1; Mismatches
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R APPLICATION NUMBER: USO1/01339
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R APPLICATION NUMBER: USO1/01348
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R EILING DATE: 2001-01-17
R APPLICATION NUMBER: USO1/01347
R FILING DATE: 2001-01-17
R APPLICATION NUMBER: USO1/01377
R R FILING DATE: 2001-01-17
R APPLICATION NUMBER: USO1/01377
R R FILING DATE: USO1/01307
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ING DATE: 2001-01-17
LICATION NUMBER: 09/764,874
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FILING DATE: 2001-01-17
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FILING DATE: 2001-01-17
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FILING DATE: 2001-01-17
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FILING DATE: 2001-01-17
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FILING DATE: 2001-01-17
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FILING DATE: 2001-01-17
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FILING DATE: 2001-01-17
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FILING DATE: 2001-01-17
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FILING DATE: 2001-01-17
APPLICATION NUMBER: 09/764,853
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110 SNVTSTSGHSSGSS 123
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Best Local Similarity 64.3
Matches 9; Conservative
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US-09-908-711-69
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CURRENT APPLICATION NUMBER: US/10/028,072 CURRENT FILING DATE: 2001-12-19
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R FILING DATE: 1997-08-26
IR APPLICATION NUMBER: 60/059113
JR FILING DATE: 1997-09-17
DR APPLICATION NUMBER: 60/059115
                                                        Sequence 196, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURKENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062814
FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/062816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059122
FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/059263
FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/059352
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APPLICATION NUMBER: 60/059836
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APPLICATION UNBER: 60/062250
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062285
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FILING DATE: 1997-10-24
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FILING DATE: 1997-10-31
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APPLICATION NUMBER: 60/053329
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APPLICATION NUMBER: 60/062287
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APPLICATION NUMBER: 60/063561
                                                                                                                                                                                                                                                                                                                                                            Stewart, Timothy A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1997-09-19
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                                                                                                                                                                                                                                            Gerritsen, Mary E.
                                                                                                                      Baker, Kevin P.
Beresini, Maureen
                                                                                                                                                                                Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                       Sherwood, Steven
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe, Colin
Wood, William
                                                                                                                                                                                                                                                                                                      Gurney, Austin I
                                                                                                                                                                                                                                                             Goddard, Audrey
                                                                                                                                                                                                                   Gao, Wei-Qiang
                                                                                                                                                                                                                                                                               Godowski, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                             DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                   Tumas,Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
FILE REFERENCE:
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Pred. No. 95;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 9; Length 335; Pred. No. 1e+02;
                                                                          MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Microbial Technics Limited
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Gilbert, Christophe FG
APPLICANT: Gilbert, Christophe FG
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT APPLICATION NUMBER: GB 9816337.1
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 388
SOFFWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                           FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, A. ANGER:
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-765-272-12
                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pneumoniae US-09-769-787-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 312 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09769787 Publication No. US20030091577A1 GENERAL INFORMATION:
                                                                                                                                      SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                        COMPUTER READABLE FORM:
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98 TSGIISRKSDNVS 110
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|121 TSGIISRKSDNVS 133
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Best Local Similarity 61.5
Matches 8; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
STATE: Maryland
                    COUNTRY: USA
ZIP: 20850
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LENGTH: 335
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RESULT 15
US-10-121-049-196
US-10-121-049-196

Sequence 196, Application US/10121049
Publication No. US20030022239A1
GENERAL INFORMATION:

seq55-247-68.rapb

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APPLICANT: Deresini, Maureen
APPLICANT: Deresini, Maureen
APPLICANT: Deresini, Mary E.
APPLICANT: Deresini, Mary E.
APPLICANT: Deroser, Luc
APPLICANT: Gao, Mary E.
APPLICANT: Gao, Mary E.
APPLICANT: Gaodwaki, Paul J.
APPLICANT: Gaodwaki, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Watanabe, Colin K
APPLICANT, Watanabe, Colin K
APPLICANT, Watanabe, Colin K
APPLICAN
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Search completed: July 15, 2003, 16:34:36 Job time: 23 secs THIS PAGE BLANK (USPTO)